

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 2, 2004, 14:51:15 ; Search time 1426 Seconds  
(without alignments)  
1550.137 Million cell updates/sec

Title: US-10-068-067-16  
Perfect score: 51  
Sequence: 1 ggtaccactggtctcttctgt.....caagaacttatcgaaataca 51

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Result No.	Score	Query Match	Length	DB	ID	Description
1	51	100.0	51	6	AX513217	AX513217 Sequence
2	51	100.0	51	6	AX513222	AX513222 Sequence
3	51	100.0	348	9	AF262299	Homo sapi
4	51	100.0	957	9	AF224496	Homo sapi
5	51	100.0	1453	9	AF247360	Homo sapi
6	51	100.0	2895	6	AX513212	Sequence
7	51	100.0	2895	9	AF237380	Homo sapi
8	51	100.0	177334	9	AC138069	Homo sapi
9	51	100.0	192729	9	AC104439	Homo sapi
10	51	100.0	220965	2	HSJ12888	
11	49.4	96.9	1454	9	AF247359	Homo sapi
12	48	94.1	260	9	AF224495	Homo sapi
13	48	94.1	406	9	AF262301	Homo sapi
14	48	94.1	410	9	AF262302	Homo sapi
15	47	92.2	212	9	AF262303	Homo sapi
16	47	92.2	436	9	AF262304	Homo sapi
17	35	68.6	1193	6	AR300122	Sequence
18	35	68.6	1193	6	BD082061	G-protein
19	26.4	51.8	41270	3	CEI1086	
20	25.8	50.6	3892	12	ECCFVIAB	
21	25.8	50.6	7907	1	AY282413	Citrobact
22	25.8	50.6	17007	1	AF316551	Citrobact
23	25.6	50.2	21362	2	AC130869	Rattus no
24	25.6	50.2	276975	2	AC106673	Rattus no
25	25.4	49.8	31059	9	AC009005	Homo sapi
26	25.4	49.8	32074	9	AC011556	Homo sapi
27	25.4	49.8	292420	2	AC020873	Mus muscu
28	25	49.0	174069	2	AC026852	Homo sapi
29	25	49.0	177929	9	AC125624	Homo sapi
30	24.6	48.2	1533	3	AK116158	Ciona int
31	24.6	48.2	69334	2	AC007778	Homo sapi
32	24.6	48.2	181250	9	AC090403	Homo sapi
33	24.6	48.2	181712	2	AP001103	Homo sapi
34	24.6	48.2	184026	9	AC022176	Homo sapi
35	24.6	48.2	186458	5	AL929391	Zebrafish
36	24.6	48.2	191312	2	AP001030	Homo sapi
37	24.6	48.2	194633	2	AC090362	Homo sapi
38	24.4	47.8	323	11	KLJ9884	Kluyverom
39	24.4	47.8	157325	9	AC027189	Homo sapi
40	24.4	47.8	163157	9	AC099784	Homo sapi
41	24.4	47.8	231772	2	AC117860	Rattus no
42	24.4	47.8	259236	2	AC123741	Mus muscu
43	24.2	47.5	157180	8	NCB18D24	Neurospor
44	24	47.1	218710	2	AC147438	Gallus ga
45	24	47.1	233527	10	AC124576	Mus muscu

ALIGNMENTS

RESULT 1  
AX513217  
LOCUS  
DEFINITION Sequence 16 from Patent WO02062848.  
ACCESSION AX513217  
VERSION AX513217.1 GI:23504280  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM  
REFERENCE  
1  
AUTHORS Rotherberg, M.E. and Zimmerman, N.  
TITLE Regulation of cc chemokine receptor 3 (ccr3) expression  
JOURNAL Patent: WO 02062848-A 16 15-AUG-2002;

AX513217 51 bp DNA linear PAT 03-OCT-2002  
Sequence 16 from Patent WO02062848.  
AX513217  
AX513217.1 GI:23504280  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
Rotherberg, M.E. and Zimmerman, N.  
Regulation of cc chemokine receptor 3 (ccr3) expression  
Patent: WO 02062848-A 16 15-AUG-2002;

Pred. No. is the number of results predicted by chance to have a

## CHILDREN'S HOSPITAL MEDICAL CENTER (US)

## FEATURES

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Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GGTACCACTGGTCTTCTGTGCTTATCCGGGCAAGAACTTATCGAAATACA 51

RESULT 2  
AX513222 51 bp RNA linear PAT 03-OCT-2002  
LOCUS  
DEFINITION Sequence 21 from Patent WO02062848.  
ACCESSION AX513222  
VERSION AX513222.1 GI:23504285  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM

REFERENCE  
AUTHORS Rothenberg, M.E. and Zimmerman, N.  
TITLE Regulation of cc chemokine receptor 3 (ccr3) expression  
JOURNAL Patent: WO 02062848-A 21 15-AUG-2002;  
CHILDREN'S HOSPITAL MEDICAL CENTER (US)

## FEATURES

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Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GGTACCACTGGTCTTCTGTGCTTATCCGGGCAAGAACTTATCGAAATACA 51

RESULT 3  
AF262299 348 bp mRNA linear PRI 26-JUN-2002  
LOCUS  
DEFINITION Homo sapiens clone 1 CC chemokine receptor 3 (CCR3) mRNA, partial cds.

ACCESSION AF262299  
VERSION AF262299.1 GI:19171640  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Vijh, S., Dayhoff, D.E., Wang, C.E., Iman, Z., Ehrenberg, P.K. and Michael, N.L.  
TITLE Transcription Regulation of Human Chemokine Receptor CCR3: Evidence for a Rare TATA-less Promoter Structure Conserved between Drosophila and Humans

JOURNAL Genomics 80 (1), 86-95 (2002)  
MEDLINE 22074933  
PUBMED 12079287  
REFERENCE 2 (bases 1 to 348)  
AUTHORS Vijh, S., Dayhoff, D.E., Wang, C.E., Ehrenberg, P.K. and Michael, N.L.  
TITLE Direct Submission

## JOURNAL

Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis,  
Walter Reed Army Institute of Research, 1600 E. Gude Drive,  
Rockville, MD 20850, USA.

## FEATURES

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Best Local Similarity 100.0%; Pred. No. 4.5e-09;  
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Qy 1 GGTACCACTGGTCTTCTGTGCTTATCCGGGCAAGAACTTATCGAAATACA 51  
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## RESULT 4

## AF224496S1

LOCUS AF224496S1 957 bp DNA linear PRI 02-MAY-2001  
DEFINITION Homo sapiens CC chemokine receptor 3 (CCR3) gene, exon 1.

ACCESSION AF224496  
VERSION AF224496.1 GI:13924485

## KEYWORDS

1 of 2  
Homo sapiens (human)

## SOURCE

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 957)  
Scotet, E.J.

## AUTHORS

## TITLE

CCR3 expression is associated with chromatin remodeling in Th2 cells

## JOURNAL

Unpublished

## REFERENCE

2 (bases 1 to 957)  
Scotet, E.J.

## AUTHORS

## TITLE

Direct Submission

## JOURNAL

Submitted (13-JAN-2000) Basel Institute for Immunology, 487 Grenzacherstrasse, Basel CH-4005, Switzerland

## FEATURES

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Db 295 GGTACCACTGGTCTCTTGTGCTTATCCGGGCAAGAACTTATCGAAATACA 345

RESULT 5
AF247360 1453 bp DNA linear PRI 26-JUN-2002
DEFINITION Homo sapiens CC chemokine receptor 3 (CCR3) gene, promoter region
and partial sequence.
ACCESSION AF247360
VERSION AF247360.1 GI:19110541
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1453)
AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Inam,Z., Ehrenberg,P.K. and
Michael,N.D.
TITLE Transcription Regulation of Human Chemokine Receptor CCR3: Evidence
for a Rare TATA-less Promoter Structure Conserved between
Drosophila and Humans
JOURNAL Genomics 80 (1), 86-95 (2002)
MEDLINE 22074933
PubMed 12079287
REFERENCE 2 (bases 1 to 1453)
AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.
TITLE Direct Submission
JOURNAL Submitted (21-MAR-2000) Dept. of Mol. Diag. and Pathogenesis, U.S.
Military HIV Research Program, 1600 E. Gude Drive, Rockville, MD
20850, USA
FEATURES
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Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 4.3e-09;
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Qy 1 GGTACCACTGGTCTCTTGTGCTTATCCGGGCAAGAACTTATCGAAATACA 51
Db 1082 GGTACCACTGGTCTCTTGTGCTTATCCGGGCAAGAACTTATCGAAATACA 1132

RESULT 6
AX513212 2895 bp DNA linear PAT 03-OCT-2002
LOCUS AX513212
DEFINITION Sequence 11 from Patent WO02062849.
ACCESSION AX513212
VERSION AX513212.1 GI:23504275
KEYWORDS
SOURCE Homo sapiens (human)

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Rothenberg,M.E. and Zimmerman,N.
TITLE Regulation of cc chemokine receptor 3 (ccr3) expression
JOURNAL Patent: WO 02062848-A 11 15-AUG-2002;
CHILDREN'S HOSPITAL MEDICAL CENTER (US)
FEATURES
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Best Local Similarity 100.0%; Pred. No. 4.2e-09;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTACCACTGGTCTCTTGTGCTTATCCGGGCAAGAACTTATCGAAATACA 51
Db 1561 GGTACCACTGGTCTCTTGTGCTTATCCGGGCAAGAACTTATCGAAATACA 1611

RESULT 7
AF237380S1 2895 bp DNA linear PRI 05-OCT-2000
LOCUS AF237380S1
DEFINITION Homo sapiens CCR3 gene, promoter and exon 1.
ACCESSION AF237380
VERSION AF237380.1 GI:10643652
KEYWORDS
SEGMENT 1 of 2
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2895)
AUTHORS Zimmermann,N., Daugherty,B.L., Kavanaugh,J.L., El-Awar,F.Y.,
Moulton,E.A. and Rothenberg,M.E.
TITLE Analysis of the CC chemokine receptor 3 gene reveals a complex 5'
exon organization, a functional role for untranslated exon 1, and a
broadly active promoter with eosinophil-selective elements
JOURNAL Blood 96 (7), 2346-2354 (2000)
MEDLINE 20458773
PubMed 11001881
REFERENCE 2 (bases 1 to 2895)
AUTHORS Daugherty,B.L.
TITLE Direct Submission
JOURNAL Submitted (22-FEB-2000) Immunology & Rheumatology, Merck Research
Laboratories, 126 East Lincoln Avenue, Rahway, NJ 07065, USA
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1287..1292
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ORIGIN

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RESULT 8  
 AC138069 177334 bp DNA linear PRI 19-FEB-2003  
 LOCUS Homo sapiens chromosome 3 clone RP13-54612, complete sequence.  
 DEFINITION  
 AC138069  
 ACCESSION  
 VERSION AC138069.3 GI:28416170  
 KEYWORDS HTG.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 177334)  
 Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,  
 Saenphimmachak,C., Buckley,D., Kibukawa,M., Raymond,C. and  
 Haugen,E.D.  
 AUTHORS Direct Submission  
 TITLE Unpublished  
 JOURNAL 2 (bases 1 to 177334)  
 REFERENCE Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.  
 AUTHORS Direct Submission  
 TITLE Submitted (12-DEC-2002) Genome Center, University of Washington,  
 JOURNAL Box 352145, Seattle, WA 98195, USA  
 REFERENCE 3 (bases 1 to 177334)  
 Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.  
 AUTHORS Direct Submission  
 TITLE Submitted (10-JAN-2003) Genome Center, University of Washington,  
 JOURNAL Box 352145, Seattle, WA 98195, USA  
 REFERENCE 4 (bases 1 to 177334)  
 Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,  
 Saenphimmachak,C., Buckley,D., Kibukawa,M., Raymond,C. and  
 Haugen,E.D.  
 AUTHORS Direct Submission  
 TITLE Submitted (19-FEB-2003) Genome Center, University of Washington,  
 JOURNAL Box 352145, Seattle, WA 98195, USA  
 COMMENT On Feb 19, 2003 this sequence version replaced gi:27573398.  
 ----- Genome Center  
 Center: University of Washington Genome Center  
 Center Code: UWGC  
 Web site: http://www.genome.washington.edu  
 Contact: uwgctgs@u.washington.edu  
 ----- Project Information  
 Center project name: chr-3  
 Center clone name: RP13-54612 (bc0820)  
 ----- Summary Statistics  
 Sequencing vector: plasmid; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.990319  
 Consensus quality: 177210 bases at least Q40  
 Consensus quality: 177313 bases at least Q30  
 Consensus quality: 177334 bases at least Q20  
 Insert size: 177334; sum-of-contigs  
 Quality coverage: 9.3x in Q20 bases; sum-of-contigs  
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 Overlapping Sequences:  
 5': RP11-793E15 (UWGC:bc0564) AC104439, 95469-bp overlap  
 3': U95626, 42710-bp overlap  
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 Sequence Quality Assessment:  
 This entry has been annotated with sequence quality  
 estimates computed by the Phrap assembly program.  
 All manually edited bases have been reduced to quality zero.  
 Quality levels above 40 are expected to have less than  
 1 error in 10,000 bp.  
 Base-by-base quality values are not generally visible from the

GenBank flat file format but are available as part  
 of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted:  
 all regions were either double-stranded or sequenced with an  
 alternate chemistry or covered by high quality data (i.e., Phred  
 quality >= 30); an attempt was made to resolve all sequencing  
 problems, such as compressions and repeats; all regions were  
 covered by at least one plasmid subclone or more than one M13  
 subclone; and the assembly was confirmed by restriction digest.

## Sequence Validation:

This sequence has been validated by Multiple Complete Digest  
 fingerprinting. Comparison of the experimentally derived digest  
 fragments with sequence-predicted fragments is given below.  
 The electronically-digested sequence consists of both insert and  
 vector, in order to accurately represent the entire circular BAC.  
 Small fragments below a variable cutoff (approximately 400-800 bp),  
 are not resolved in the fingerprint and hence do not appear  
 in the table. There are no significant remaining discrepancies  
 between the experimental and predicted values. Uniquely ordered  
 fragments are separated by dashed lines.

EcoRI

HindIII

BglII

SeqDerMap	FrgrPrnt	SeqDerMap	FrgrPrnt	SeqDerMap	FrgrPrnt
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10424	10027	4052	4034	875	893
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7015	7139	219	<800	3835	3756
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2737	2749	2752	2834	685	<800
3448	3416	1647	1641	2598	2662
3256	3238	7059	7056	248	<800
5801	5759	1547	1503	2152	2210
1512	1497	5163	5136	431	<800
1398	1392	8679	8719	237	<800
8413	8333	2033	2035	3380	3411
6621	6614	886	892	5694	5744
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Query Match 100.0%; Score 51; DB 9; Length 177334;  
Best Local Similarity 100.0%; Pred. No. 3.6e-09;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACACTGGCTCTTCTTGCTTATCCGGGAAGAACTATCGAATACA 51  
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DB 65693 GGTACACTGGCTCTTCTTGCTTATCCGGGAAGAACTATCGAATACA 65743  
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RESULT 9  
AC104439  
LOCUS  
DEFINITION  
AC104439 AC024739  
AC104439.2 GI:21490240  
VERSION  
KEYWORDS  
HTG.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 197279)  
Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,  
Saenphimmachak,C., Phelps,K.A., Buckley,D., Kibukawa,M., Raymond,C.  
and Haugen,E.D.  
Direct Submission  
Unpublished  
2 (bases 1 to 197279)  
Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.  
Direct Submission  
Submitted (11-DEC-2001) Genome Center, University of Washington,  
Box 352145, Seattle, WA 98195, USA  
3 (bases 1 to 197279)  
Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,  
Saenphimmachak,C., Phelps,K.A., Buckley,D., Kibukawa,M., Raymond,C.  
and Haugen,E.D.  
Direct Submission  
Submitted (20-JUN-2002) Genome Center, University of Washington,  
Box 352145, Seattle, WA 98195, USA  
On Jun 20, 2002 this sequence version replaced gi:17488621.  
----- Genome Center  
Center: University of Washington Genome Center  
Center Code: UWGC  
Web site: http://www.genome.washington.edu  
Contact: uwgchtgs@u.washington.edu  
Drafting Center: WUGSC  
----- Project Information  
Center project name: chr-3  
Center clone name: RP11-793E15 (bc0564)  
----- Summary Statistics  
Sequencing vector: unknown; 52% of reads  
Chemistry: Dye-terminator ET; 94% of reads  
Chemistry: Dye-terminator Big Dye; 6% of reads  
Assembly program: Phrap; version 0.990319  
Consensus quality: 197168 bases at least Q40  
Consensus quality: 197255 bases at least Q30  
Consensus quality: 197275 bases at least Q20  
Insert size: 197279; sum-of-contigs  
Quality coverage: 8.2x in Q20 bases; sum-of-contigs  
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Overlapping Sequences:  
5': RP11-91E8 (UWGC:bc0216) AC026349  
3': CTD-2563A18 (UWGC:bc0730)  
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Sequence Quality Assessment:  
This entry has been annotated with sequence quality  
estimates computed by the Phrap assembly program.  
All manually edited bases have been reduced to quality zero.  
Quality levels above 40 are expected to have less than  
1 error in 10,000 bp.  
Base-by-base quality values are not generally visible from the  
GenBank flat file format but are available as part  
of this entry's ASN.1 file.  
-----  
This sequence was finished as follows unless otherwise noted:  
all regions were either double-stranded or sequenced with an  
alternate chemistry or covered by high quality data (i.e., phred  
quality >= 30); an attempt was made to resolve all sequencing  
problems, such as compressions and repeats; all regions were  
covered by at least one plasmid subclone or more than one M13

subclone; and the assembly was confirmed by restriction digest.

#### Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

HindIII				BglII				EcoRI			
SeqDerMap	FrngPrnt	SeqDerMap	FrngPrnt	SeqDerMap	FrngPrnt	SeqDerMap	FrngPrnt	SeqDerMap	FrngPrnt	SeqDerMap	FrngPrnt
2687	2617	8949	8586	8996	8661						
6382	6410	2067	2160	6	<800						
512	<800	7846	7940	2742	2803						
449	<800	3734	3895	5376	5324						
2602	2763	1334	1301	1493	1478						
2590	2617	2287	2309	823	835						
8313	8291	1814	1918	1962	2002						
1711	1683	691	<800	2900	2954						
9821	9472	5477	5348	1484	1478						
516	<800	305	<800	1005	995						
8587	8291	25245	25541	1181	1171						
7446	7581	3988	4121	18560	19002						
2088	2075	1633	1598	3603	3579						
2509	2617	631	<800	4943	5076						
3519	3501	90	<800	3239	3241						
26	<800	402	<800	953	995						
925	933	3350	3490	1621	1615						
98	<800	4577	4515	6827	6900						
6409	6410	1229	1183	79	<800						
1383	1376	4221	4331	16418	16263						
16048	15829	3980	4121	3361	3241						
1876	1877	2548	2497	872	881						
4169	4068	674	<800	4220	4193						
1674	1683	2332	2309	2848	2803						
52	<800	11445	11045	2283	2318						
5227	5082	5692	5632	3211	3241						
15464	15829	1385	1414	4615	4632						

14333	14296	608	<800	6823	6900
1026	1026	3930	3895	886	881
645	<800	1465	1414	2032	2002
6621	6410	2382	2497	8680	8661
8413	8291	747	<800	5163	5076
1401	1376	1951	2012	1547	1478
1512	1471	642	<800	7058	6900
5801	5644	21060	21003	1647	1615
3256	3278	3700	3666	2753	2803
3448	3501	1321	1301	162	<800
2738	2763	10705	10502	1078	1093
237	<800	3128	3317	2156	2173
6715	6823	183	<800	5077	5076
201	<800	3255	3490	154	<800
1002	1026	5693	5632	1571	1478
221	<800	3380	3317	219	<800
2854	2899	237	<800	520	<800
6998	7317	431	<800	1540	1478
1174	1145	2152	2160	1479	1478
7876	8291	249	<800	1613	1615
1911	1877	2599	2778	1399	1478
3899	3847	685	<800	9553	9383
5672	5644	41	<800	166	<800
1711	1683	388	<800	13615	13115
862	854	2500	2497	4731	4632
2368	2389	2889	2778	5159	5076
		178	<800	4503	4430
		6589	6728	6607	6900
		3836	3895	2766	2803

Query Match 100.0%; Score 51; DB 9; Length 197279;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-09;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTACCACTGGTCTCTTGTGCTTATCCGGGCAAGAACTTATCGAAATACA 51

Db 167486 GGTACCACTGGTCTCTTGTGCTTATCCGGGCAAGAACTTATCGAAATACA 167536

RESULT 10

HSA312688

LOCUS

DEFINITION

SEQUENCING IN PROGRESS \*\*\*

220965 bp

DNA

linear

HTG 15-MAY-2002

Homo sapiens chromosome 3 clone RP6-32g23 map 3p21.3, \*\*\*

26 ordered pieces.

AJ312688  
 VERSION AJ312688.2 GI:13559235  
 KEYWORDS HTG: HTGS\_PHASE2.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1  
 Kiss, H., Yang, Y., Kiss, C., Andersson, K., Klein, G., Imreh, S. and  
 Dumas, J.P.  
 TITLE The transcriptional map of the common eliminated region 1 (C3CER1)  
 in 3p21.3  
 Eur. J. Hum. Genet. 10 (1), 52-61 (2002)  
 JOURNAL 21906202  
 MEDLINE 21906202  
 PUBMED 11896456  
 REFERENCE 2 (bases 1 to 220965)  
 AUTHORS Kiss, H.  
 DIRECT SUBMISSION  
 SUBMITTED (01-APR-2001) Kiss H., Microbiology and Tumourbiology  
 Center (MTC), Karolinska Institute, Box 280, Stockholm, S-17177,  
 SWEDEN  
 COMMENT On Apr 5, 2001 this sequence version replaced gi:13548633.  
 The sequence is a consensus sequence of clone RP4-787c23 (1-140400  
 bp),  
 clone RP6-32g23 (31212-220965 bp), clone RP6-146e1 (partially,  
 1-6800 bp)  
 and clone RP6-188g11 (partially, 1-108303 bp). The sequencing  
 contigs are  
 in order and the gaps between them are represented by 100 Ns.  
 Contig 1:  
 1-11731 bp Contig 2: 11832-26218 bp Contig 3: 26319-28347 bp  
 Contig 4:  
 28448-42160 bp Contig 5: 42261-55059 bp Contig 6: 55160-61578 bp  
 Contig  
 7: 61679-97342 bp Contig 8: 97443-117655 bp Contig 9:  
 117756-118727 bp  
 Contig 10: 118828-121834 bp Contig 11: 121935-127855 bp Contig  
 12:  
 127956-129383 bp Contig 13: 129484-131747 bp Contig 14:  
 131848-132316 bp  
 Contig 15: 132417-134455 bp Contig 16: 134556-135527 bp Contig  
 17:  
 135628-189051 bp Contig 18: 189152-189476 bp Contig 19:  
 189577-191375 bp  
 Contig 20: 191476-201473 bp Contig 21: 201574-202307 bp Contig  
 22:  
 202408-204878 bp Contig 23: 204979-213531 bp Contig 24:  
 213632-218109 bp  
 Contig 25: 218210-219800 bp Contig 26: 219901-220965 bp.  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 26 contigs. Gaps between the contigs  
 \* are represented as runs of N. The order of the pieces  
 \* is believed to be correct as given, however the sizes  
 \* of the gaps between them are based on estimates that have  
 \* provided by the submitter.  
 \* This sequence will be replaced  
 \* by the finished sequence as soon as it is available and  
 \* the accession number will be preserved.  
 1  
 11731: contig of 11731 bp in length  
 \* 11732 11831: gap of 100 bp  
 \* 11832 26218: contig of 14387 bp in length  
 \* 26219 26318: gap of 100 bp  
 \* 26319 28347: contig of 2029 bp in length  
 \* 28348 28447: gap of 100 bp  
 \* 28448 42160: contig of 13713 bp in length  
 \* 42161 42360: gap of 200 bp  
 \* 42361 55059: contig of 12699 bp in length  
 \* 55060 55159: gap of 100 bp  
 \* 55160 61578: contig of 6419 bp in length  
 \* 61579 61678: gap of 100 bp  
 \* 61679 97342: contig of 35664 bp in length  
 \* 97343 97443: gap of 100 bp  
 \* 97443 117655: contig of 20213 bp in length

\* 117656 117755: gap of 100 bp  
 \* 117756 118727: contig of 972 bp in length  
 \* 118728 118827: gap of 100 bp  
 \* 118828 121834: contig of 3007 bp in length  
 \* 121835 121934: gap of 100 bp  
 \* 121935 127855: contig of 5921 bp in length  
 \* 127856 127955: gap of 100 bp  
 \* 127956 129383: contig of 1428 bp in length  
 \* 129384 129484: gap of 100 bp  
 \* 129484 131747: contig of 2264 bp in length  
 \* 131748 131847: gap of 100 bp  
 \* 131848 132316: contig of 469 bp in length  
 \* 132317 132416: gap of 100 bp  
 \* 132417 134455: contig of 2039 bp in length  
 \* 134456 134555: gap of 100 bp  
 \* 134556 135527: contig of 972 bp in length  
 \* 135528 135627: gap of 100 bp  
 \* 135628 189051: contig of 53424 bp in length  
 \* 189052 189151: gap of 100 bp  
 \* 189152 189476: contig of 325 bp in length  
 \* 189477 189577: gap of 100 bp  
 \* 189578 191375: contig of 1799 bp in length  
 \* 191376 191475: gap of 100 bp  
 \* 191476 201473: contig of 998 bp in length  
 \* 201474 201573: gap of 100 bp  
 \* 201574 202307: contig of 734 bp in length  
 \* 202308 202407: gap of 100 bp  
 \* 202408 204878: contig of 2471 bp in length  
 \* 204879 204978: gap of 100 bp  
 \* 204979 213531: contig of 8553 bp in length  
 \* 213532 213631: gap of 100 bp  
 \* 213632 218109: contig of 4478 bp in length  
 \* 218110 218209: gap of 100 bp  
 \* 218210 219800: contig of 1591 bp in length  
 \* 219801 219900: gap of 100 bp  
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 Best Local Similarity 100.0%; Pred. No. 3,6e-09;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GGTACCACTGGTCTCTTGTGCTTATCCGGGCAAGAACTTATCGAATACA 51  
 Db 121110 GGTACCACTGGTCTCTTGTGCTTATCCGGGCAAGAACTTATCGAATACA 121160  
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 AF247359 Homo sapiens CC chemokine receptor 3 (CCR3) gene, promoter region  
 LOCUS AF247359 1454 bp DNA linear PRI 26-JUN-2002  
 DEFINITION Homo sapiens CC chemokine receptor 3 (CCR3) gene, promoter region  
 and partial sequence.  
 ACCESSION AF247359  
 VERSION AF247359.1 GI:191110540  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
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 1 (bases 1 to 1454)  
 REFERENCE Vijn, S., Dayhoff, D.E., Wang, C.E., Imam, Z., Ehrenberg, P.K. and  
 Michael, N.L.  
 AUTHORS Transcription Regulation of Human Chemokine Receptor CCR3: Evidence  
 for a Rare TATA-less Promoter Structure Conserved between  
 Drosophila and Humans

JOURNAL Genomics 80 (1), 86-95 (2002)  
 MEDLINE 22074933  
 PUBMED 12079287  
 REFERENCE 2 (bases 1 to 1454)  
 AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.  
 TITLE Direct Submission  
 JOURNAL Submitted (21-MAR-2000) Dept. of Mol. Diag. and Pathogenesis, U.S. Military HIV Research Program, 1600 E. Gude Drive, Rockville, MD 20850, USA

FEATURES  
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gene  
 variation

mRNA

exon  
 variation

ORIGIN

Query Match 96.9%; Score 49.4; DB 9; Length 1454;  
 Best Local Similarity 98.0%; Pred. No. 1.8e-08;  
 Matches 50; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTACCACTGGTCTTCTTGCTTATCCGGGCAAGAACTTATCGAATACA 51  
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 Db 1083 GGTACCACTGGTCTTCTTGCTTATCCGGGCGAGAACTTATCGAATACA 1133  
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RESULT 12  
 AF224495 260 bp mRNA linear PRI 02-MAY-2001  
 LOCUS Homo sapiens CC chemokine receptor 3 (CCR3) mRNA, partial cds.  
 DEFINITION  
 ACCESSION AF224495  
 VERSION AF224495.1 GI:113924481  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 260)  
 AUTHORS Scotet,E.J.  
 TITLE CCR3 expression is associated with chromatin remodeling in Th2 cells  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 260)  
 AUTHORS Scotet,E.J.  
 TITLE Direct Submission  
 JOURNAL Submitted (13-JAN-2000) Basel Institute for Immunology, 487 Grenzacherstrasse, Basel CH-4005, Switzerland

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ORIGIN

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QY 4 ACCACTGGTCTTCTTGCTTATCCGGGCAAGAACTTATCGAATACA 51  
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 Db 1 ACCACTGGTCTTCTTGCTTATCCGGGCAAGAACTTATCGAATACA 48  
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RESULT 13  
 AF262301 406 bp mRNA linear PRI 26-JUN-2002  
 LOCUS Homo sapiens clone 4 CC chemokine receptor 3 (CCR3) mRNA, partial cds.  
 DEFINITION  
 ACCESSION AF262301  
 VERSION AF262301.1 GI:19171644  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 406)  
 AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and Michael,N.L.  
 TITLE Transcription Regulation of Human Chemokine Receptor CCR3: Evidence for a Rare ThA-Less Promoter Structure Conserved between Drosophila and Humans  
 JOURNAL Genomics 80 (1), 86-95 (2002)  
 MEDLINE 12079287  
 PUBMED 12079287  
 REFERENCE 2 (bases 1 to 406)  
 AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.  
 TITLE Direct Submission  
 JOURNAL Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis, Walter Reed Army Institute of Research, 1600 E. Gude Drive, Rockville, MD 20850, USA

FEATURES  
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gene  
 CDS

ORIGIN

Query Match 94.1%; Score 48; DB 9; Length 406;  
 Best Local Similarity 100.0%; Pred. No. 6.8e-08;  
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 14
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LOCUS Homo sapiens clone 5 CC chemokine receptor 3 (CCR3) mRNA, partial
DEFINITION cds.
ACCESSION AF262302
VERSION AF262302.1 GI:19171646
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 410)
AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and
Michael,N.L.
TITLE Transcription Regulation of Human Chemokine Receptor CCR3: Evidence
for a Rare TATA-less Promoter Structure Conserved between
Drosophila and Humans
JOURNAL Genomics 80 (1), 86-95 (2002)
MEDLINE 22074933
PUBMED 12079287
SOURCE 2 (bases 1 to 410)
AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.
DIRECT SUBMISSION
TITLE Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis,
Walter Reed Army Institute of Research, 1600 E. Gude Drive,
Rockville, MD 20850, USA
JOURNAL
FEATURES
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monocytes"
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Best Local Similarity 100.0%; Pred. No. 6.8e-08;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ACCACTGGTCTCTTGTCATTATCCGGCGAAGAACTTATCGAATACA 48
|||||

RESULT 15
AF262303 212 bp mRNA linear PRI 26-JUN-2002
LOCUS Homo sapiens clone 6 CC chemokine receptor 3 (CCR3) mRNA, partial
DEFINITION cds.
ACCESSION AF262303
VERSION AF262303.1 GI:19171648
KEYWORDS

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 212)
AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and
Michael,N.L.
TITLE Transcription Regulation of Human Chemokine Receptor CCR3: Evidence
for a Rare TATA-less Promoter Structure Conserved between
Drosophila and Humans
JOURNAL Genomics 80 (1), 86-95 (2002)
MEDLINE 22074933
PUBMED 12079287
SOURCE 2 (bases 1 to 212)
AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.
DIRECT SUBMISSION
TITLE Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis,
Walter Reed Army Institute of Research, 1600 E. Gude Drive,
Rockville, MD 20850, USA
JOURNAL
FEATURES
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/chromosome="3"
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CD8 lymphocytes, microglia, dendritic cells, and
monocytes"
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Best Local Similarity 100.0%; Pred. No. 1.7e-07;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCACGTGCTTCTTGTCATTATCCGGCGAAGAACTTATCGAATACA 51
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Db 1 CCACGTGCTTCTTGTCATTATCCGGCGAAGAACTTATCGAATACA 47
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Search completed: August 2, 2004, 16:55:33
Job time : 1437 secs
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 212)
AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and
Michael,N.L.
TITLE Transcription Regulation of Human Chemokine Receptor CCR3: Evidence
for a Rare TATA-less Promoter Structure Conserved between
Drosophila and Humans
JOURNAL Genomics 80 (1), 86-95 (2002)
MEDLINE 22074933
PUBMED 12079287
SOURCE 2 (bases 1 to 212)
AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.
DIRECT SUBMISSION
TITLE Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis,
Walter Reed Army Institute of Research, 1600 E. Gude Drive,
Rockville, MD 20850, USA
JOURNAL
FEATURES
source
1..212
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="3"
/map="3p21"
/clone="6"
1..212
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150..212
/gene="CCR3"
/note="G-protein coupled receptor; principal eotaxin
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CD8 lymphocytes, microglia, dendritic cells, and
monocytes"
/codon_start=1
/product="CC chemokine receptor 3"
/protein_id="AAL85632.1"
/db_xref="GI:19171649"
/translation="MTSLDTVETFGTTSYDDVG"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.7e-07;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCACGTGCTTCTTGTCATTATCCGGCGAAGAACTTATCGAATACA 51
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Db 1 CCACGTGCTTCTTGTCATTATCCGGCGAAGAACTTATCGAATACA 47
|||||

Search completed: August 2, 2004, 16:55:33
Job time : 1437 secs
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**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 2, 2004, 17:27:15 ; Search time 1142.66 Seconds  
(without alignments)  
1934.510 Million cell updates/sec

Title: US-10-068-067-16

Perfect score: 51

Sequence: 1 ggtaccactggtctcttgtt.....caagaacttatcgaaataca 51

Scoring table:

OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_hg.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pi.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sv.\*

13: gb\_un.\*

14: gb\_vi.\*

15: em\_ba.\*

16: em\_fun.\*

17: em\_hum.\*

18: em\_in.\*

19: em\_mu.\*

20: em\_om.\*

21: em\_or.\*

22: em\_ov.\*

23: em\_pat.\*

24: em\_ph.\*

25: em\_pl.\*

26: em\_ro.\*

27: em\_sts.\*

28: em\_un.\*

29: em\_vi.\*

30: em\_htg\_hum.\*

31: em\_htg\_inv.\*

32: em\_htg\_other.\*

33: em\_htg\_mus.\*

34: em\_htg\_pln.\*

35: em\_htg\_rtd.\*

36: em\_htg\_mam.\*

37: em\_htg\_vrt.\*

38: em\_sy.\*

39: em\_hgo\_hum.\*

40: em\_hgo\_mus.\*

41: em\_hgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	51	100.0	51	6	AX513217	AX513217 Sequence
2	51	100.0	51	6	AX513222	AX513222 Sequence
3	51	100.0	348	9	AF262299	AF262299 Homo sapi
4	51	100.0	957	9	AF224496	AF224496 Homo sapi
5	51	100.0	1453	9	AF247360	AF247360 Homo sapi
6	51	100.0	2895	6	AX513212	AX513212 Sequence
7	51	100.0	2895	9	AF237380S1	AF237380 Homo sapi
8	51	100.0	177334	9	AC138069	AC138069 Homo sapi
9	51	100.0	197279	9	AC104439	AC104439 Homo sapi
10	51	100.0	220985	2	HS312888	AJ32688 Homo sapi
11	48	94.1	260	9	AF224495	AF224495 Homo sapi
12	48	94.1	406	9	AF262301	AF262301 Homo sapi
13	48	94.1	410	9	AF262302	AF262302 Homo sapi
14	47	92.2	212	9	AF262303	AF262303 Homo sapi
15	47	92.2	436	9	AF262304	AF262304 Homo sapi
16	35	68.6	1193	6	BD082061	BD082061 G-protein
17	35	68.6	1193	6	BD082061	BD082061 G-protein
18	32	62.7	1454	9	AF247359	AF247359 Homo sapi
19	22	43.1	22	6	AX513218	AX513218 Sequence
20	22	43.1	22	6	AX513219	AX513219 Sequence
21	22	43.1	22	6	AX513224	AX513224 Sequence
22	21	41.2	21	6	AX513220	AX513220 Sequence
23	21	41.2	21	6	AX513223	AX513223 Sequence
24	21	41.2	21	6	AX513225	AX513225 Sequence
25	19	37.3	208519	10	AL669871	AL669871 Mouse DNA
26	18	35.3	31654	3	CEC32H11	282260 Caenorhabdi
27	18	35.3	121524	8	AF041468	AF041468 Guillard
28	18	35.3	173554	2	AC144357	AC144357 Dario rer
29	17	33.3	2145	8	AF180024	AF180024 Huperzia
30	17	33.3	3187	8	CHCRPS13	X05847 C.reinhardt
31	17	33.3	6991	3	PFARHPR	L27838 Plasmodium
32	17	33.3	8241	3	AF323443	AF323443 Plasmodiu
33	17	33.3	8256	3	AF323442	AF323442 Plasmodiu
34	17	33.3	58883	2	AC129517	AC129517 Homo sapi
35	17	33.3	73031	9	HS78B3	282217 Human DNA s
36	17	33.3	95556	9	HSJ73H14	AL080272 Human DNA
37	17	33.3	95613	2	AC020389	AC020389 Drosophil
38	17	33.3	112182	2	AC141177	AC141177 Rattus no
39	17	33.3	114458	10	BS293986	BS293986 Mouse DNA
40	17	33.3	128574	8	OSJN00199	AL663002 Oryza sat
41	17	33.3	137739	9	HS994L9	AL034554 Human DNA
42	17	33.3	148892	8	AP003235	AP003235 Oryza sat
43	17	33.3	155840	2	AC006495	AC006495 Drosophil
44	17	33.3	161079	2	AC083842	AC083842 Homo sapi
45	17	33.3	161826	9	AL358532	AL358532 Human DNA

#### ALIGNMENTS

RESULT 1  
AX513217  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

AX513217  
Sequence 16 from Patent WO02062848.  
AX513217  
AX513217.1 GI:23504280  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
Rothenberg, M.E. and Zimmerman, N.  
Regulation of cc chemokine receptor 3 (ccr3) expression  
Patent: WO 02062848-A 16 15-AUG-2002;

AX513217  
Sequence 16 from Patent WO02062848.  
AX513217  
AX513217.1 GI:23504280  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
Rothenberg, M.E. and Zimmerman, N.  
Regulation of cc chemokine receptor 3 (ccr3) expression  
Patent: WO 02062848-A 16 15-AUG-2002;

AX513217  
Sequence 16 from Patent WO02062848.  
AX513217  
AX513217.1 GI:23504280  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
Rothenberg, M.E. and Zimmerman, N.  
Regulation of cc chemokine receptor 3 (ccr3) expression  
Patent: WO 02062848-A 16 15-AUG-2002;

## CHILDREN'S HOSPITAL MEDICAL CENTER (US)

## FEATURES

source  
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Location/Qualifiers  
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/mol\_type="unassigned DNA"  
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## ORIGIN

Query Match 100.0%; Score 51; DB 6; Length 51;  
Best Local Similarity 100.0%; Pred. No. 2e-19;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTACCACTGGTCTTCTGTGCTTATCCGGGCAAGAACTTATCGAATACA 51  
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Db 1 GGTACCACTGGTCTTCTGTGCTTATCCGGGCAAGAACTTATCGAATACA 51

RESULT 2  
AX513222 AX513222 51 bp RNA linear PAT 03-OCT-2002  
LOCUS  
DEFINITION Sequence 21 from Patent WO02062848.  
ACCESSION AX513222  
VERSION AX513222.1 GI:23504285

## KEYWORDS

SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 Rothenberg, M.E. and Zimmerman, N.

AUTHORS Regulation of cc chemokine receptor 3 (ccr3) expression

TITLE Patent: WO 02062848-A 21 15-AUG-2002;

JOURNAL CHILDREN'S HOSPITAL MEDICAL CENTER (US)

## FEATURES

source  
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## ORIGIN

Query Match 100.0%; Score 51; DB 6; Length 51;  
Best Local Similarity 100.0%; Pred. No. 2e-19;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTACCACTGGTCTTCTGTGCTTATCCGGGCAAGAACTTATCGAATACA 51  
|||||  
Db 1 GGTACCACTGGTCTTCTGTGCTTATCCGGGCAAGAACTTATCGAATACA 51

RESULT 3  
AF262299 AF262299 348 bp mRNA linear PRI 26-JUN-2002  
LOCUS  
DEFINITION Homo sapiens clone 1 CC chemokine receptor 3 (CCR3) mRNA, partial cds.

## ACCESSION

AF262299

VERSION AF262299.1 GI:19171640

## KEYWORDS

SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 Vijh, S., Dayhoff, D.E., Wang, C.E., Iman, Z., Ehrenberg, P.K. and

AUTHORS Michael, N.L.

TITLE Transcription Regulation of Human Chemokine Receptor CCR3: Evidence

for a Rare TATA-less Promoter Structure Conserved between

Drosophila and Humans

JOURNAL Genomics 80 (1), 86-95 (2002)

## MEDLINE

22074933

PUBMED 12079287

## REFERENCE

2 (bases 1 to 348)

AUTHORS Vijh, S., Dayhoff, D.E., Wang, C.E., Ehrenberg, P.K. and Michael, N.L.

## TITLE

Direct Submission

## JOURNAL

Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis,  
Walter Reed Army Institute of Research, 1600 E. Gude Drive,  
Rockville, MD 20850, USA  
Location/Qualifiers  
1. .348

## FEATURES

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## CDS

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receptor expressed on eosinophils; CD4 Th2 lymphocytes,

CD8 lymphocytes, microglia, dendritic cells, and

monocytes"

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/protein\_id="AA185628.1"

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Query Match 100.0%; Score 51; DB 9; Length 348;  
Best Local Similarity 100.0%; Pred. No. 1.9e-19;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTACCACTGGTCTTCTGTGCTTATCCGGGCAAGAACTTATCGAATACA 51

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QY 1 GTTACACTGGTCTTCTTGCTTATCCGGGCAAGAACTTATCGAAATACA 51  
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 Db 295 GGTACCACTGGTCTTCTTGCTTATCCGGGCAAGAACTTATCGAAATACA 345

RESULT 5  
 AF247360 1453 bp DNA linear PRI 26-JUN-2002  
 LOCUS Homo sapiens CC chemokine receptor 3 (CCR3) gene, promoter region  
 DEFINITION and partial sequence.  
 ACCESSION AF247360  
 VERSION AF247360.1 GI:19110541  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1453)  
 AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and Michael,N.L.  
 TITLE Transcription Regulation of Human Chemokine Receptor CCR3: Evidence for a Rare TATA-less Promoter Structure Conserved between Drosophila and Humans  
 JOURNAL Genomics 80 (1), 86-95 (2002)  
 MEDLINE 22074933  
 PUBMED 12079287  
 REFERENCE 2 (bases 1 to 1453)  
 AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.  
 TITLE Direct Submission  
 JOURNAL Submitted (21-MAR-2000) Dept. of Mol. Diag. and Pathogenesis, U.S. Military HIV Research Program, 1600 E. Gude Drive, Rockville, MD 20850, USA

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 Best Local Similarity 100.0%; Pred. No. 1.8e-19;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTACACTGGTCTTCTTGCTTATCCGGGCAAGAACTTATCGAAATACA 51  
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 Db 1082 GGTACCACTGGTCTTCTTGCTTATCCGGGCAAGAACTTATCGAAATACA 1132

RESULT 6  
 AX513212 2895 bp DNA linear PAT 03-OCT-2002  
 LOCUS Sequence 11 from Patent WO02062848.  
 DEFINITION  
 ACCESSION AX513212  
 VERSION AX513212.1 GI:23504275  
 KEYWORDS  
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Rothenberg,M.E. and Zimmerman,N.  
 TITLE Regulation of cc chemokine receptor 3 (ccr3) expression  
 JOURNAL Patent: WO 02062848-A 11 15-AUG-2002;  
 CHILDREN'S HOSPITAL MEDICAL CENTER (US)  
 FEATURES Location/Qualifiers  
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 Db 1561 GGTACCACTGGTCTTCTTGCTTATCCGGGCAAGAACTTATCGAAATACA 1611

RESULT 7  
 AF237380S1 2895 bp DNA linear PRI 05-OCT-2000  
 LOCUS Homo sapiens CCR3 gene, promoter and exon 1.  
 DEFINITION  
 ACCESSION AF237380  
 VERSION AF237380.1 GI:10843652  
 KEYWORDS  
 SEGMENT  
 SOURCE 1 of 2  
 ORGANISM Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 2895)  
 AUTHORS Zimmermann,N., Daugherty,B.L., Kavanaugh,J.L., El-Awar,F.Y., Moulton,E.A. and Rothenberg,M.E.  
 TITLE Analysis of the CC chemokine receptor 3 gene reveals a complex 5' exon organization, a functional role for untranslated exon 1, and a broadly active promoter with eosinophil-selective elements  
 JOURNAL Blood 96 (7), 2346-2354 (2000)  
 MEDLINE 20458773  
 PUBMED 11001881  
 REFERENCE 2 (bases 1 to 2895)  
 AUTHORS Daugherty,B.L.  
 TITLE Direct Submission  
 JOURNAL Submitted (22-FEB-2000) Immunology & Rheumatology, Merck Research Laboratories, 126 East Lincoln Avenue, Rahway, NJ 07065, USA  
 FEATURES Location/Qualifiers  
 source  
 1..2895  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
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 /clone="350-3B"  
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 33..38  
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ORIGIN  
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 exon  
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Query Match 100.0%; Score 51; DB 9; Length 2895;  
 Best Local Similarity 100.0%; Pred. NO. 1.8e-19;  
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Oy 1 GGTACCACTGGTCTTCTTGCTATCCGGGCAAGACTTATCGAATACA 51  
 Db 1561 GGTACCACTGGTCTTCTTGCTATCCGGGCAAGACTTATCGAATACA 1611

## RESULT 8

AC138069 177334 bp DNA linear PRI 19-FEB-2003  
 LOCUS AC138069 Homo sapiens chromosome 3 clone RP13-54612, complete sequence.

ACCESSION AC138069  
 VERSION AC138069.3 GI:28416170  
 KEYWORDS HTG.

## SOURCE

ORGANISM Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 177334)  
 Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,  
 Saenphimmachak,C., Buckley,D., Kibukawa,M., Raymond,C. and  
 Haugen,E.D.

## REFERENCE

## AUTHORS

Direct Submission

## TITLE

Unpublished

2 (bases 1 to 177334)

## REFERENCE

## AUTHORS

Direct Submission

## TITLE

Submitted (12-DEC-2002) Genome Center, University of Washington,

## JOURNAL

Box 352145, Seattle, WA 98195, USA

## REFERENCE

## AUTHORS

3 (bases 1 to 177334)

## TITLE

Direct Submission

## JOURNAL

Submitted (10-JAN-2003) Genome Center, University of Washington,

## REFERENCE

## AUTHORS

Box 352145, Seattle, WA 98195, USA

## TITLE

4 (bases 1 to 177334)

## JOURNAL

Submitted (10-JAN-2003) Genome Center, University of Washington,

## REFERENCE

## AUTHORS

Box 352145, Seattle, WA 98195, USA

## TITLE

On Feb 19, 2003 this sequence version replaced gi:27573398.

## JOURNAL

Genome Center

## REFERENCE

## AUTHORS

Center: University of Washington Genome Center

## TITLE

Center Code: UWGC

## JOURNAL

Web site: <http://www.genome.washington.edu>

## REFERENCE

## AUTHORS

Contact: [uwgctgs@u.washington.edu](mailto:uwgctgs@u.washington.edu)

## TITLE

Project Information

## JOURNAL

Center project name: chr-3

## REFERENCE

## AUTHORS

Center clone name: RP13-54612 (bc0820)

## TITLE

Summary Statistics

Sequencing vector: plasmid; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 177210 bases at least Q40

Consensus quality: 177313 bases at least Q30

Consensus quality: 177334 bases at least Q20

Insert size: 177334; sum-of-contigs

Quality coverage: 9.3x in Q20 bases; sum-of-contigs

Overlapping Sequences:

5': RP11-793E15 (UWGC:bc0564) AC104439, 95469-bp overlap

3': U95626, 42710-bp overlap

Sequence Quality Assessment:

This entry has been annotated with sequence quality

estimates computed by the Phrap assembly program.

All manually edited bases have been reduced to quality zero.

Quality levels above 40 are expected to have less than

1 error in 10,000 bp.

Base-by-base quality values are not generally visible from the

GenBank flat file format but are available as part  
 of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted:  
 all regions were either double-stranded or sequenced with an  
 alternate chemistry or covered by high quality data (i.e., Phred  
 quality >= 30); an attempt was made to resolve all sequencing  
 problems, such as compressions and repeats; all regions were  
 covered by at least one plasmid subclone or more than one M13  
 subclone; and the assembly was confirmed by restriction digest.

## Sequence Validation:

This sequence has been validated by Multiple Complete Digest  
 fingerprinting. Comparison of the experimentally derived digest  
 fragments with sequence-predicted fragments is given below.  
 The electronically-digested sequence consists of both insert and  
 vector, in order to accurately represent the entire circular BAC.  
 Small fragments below a variable cutoff (approximately 400-800 bp)  
 are not resolved in the fingerprint and hence do not appear  
 in the table. There are no significant remaining discrepancies  
 between the experimental and predicted values. Uniquely ordered  
 fragments are separated by dashed lines.

## HindIII EcoRI

SeqDerMap	FrgrPrnt	SeqDerMap	FrgrPrnt	SeqDerMap	FrgrPrnt	BglII
1239	1199	11125	10952	6306	6319	
449	<800	2290	2310	2067	2071	
510	<800	560	<800	3913	3756	
6511	6363	54	<800	2169	2210	
5296	5509	1159	1158	910	910	
10424	10027	4052	4034	875	893	
5046	5119	1846	1829	3716	3756	
1196	1199	8334	8273	4502	4523	
1397	1392	12882	12573	1967	1945	
2597	2624	448	<800	2864	2871	
1688	1674	12737	12573	4724	4738	
3800	3818	10300	10103	4773	4738	
2248	2269	6671	6656	3707	3756	
1074	1055	4052	4034	336	<800	
7303	7718	1392	1386	79	<800	
959	959	4253	4286	4736	4738	
551	<800	2791	2834	1889	1945	
1074	1055	2647	2682	3696	3756	
5688	5759	3423	3409	1569	1539	
5183	5363	73	<800	8078	8038	
3100	3093	499	<800	1365	1325	
921	959	723	<800	289	<800	
4350	4244	2763	2834	11047	10790	

4931	4857	6594	6656	8848	8963
3907	3818	4503	4468	1914	1945
8001	7718	5154	5136	1336	1325
3804	3818	4730	4713	11485	11341
2355	2376	13628	13324	974	975
862	868	166	<800	2448	2501
1711	1674	9554	9494	373	<800
5672	5759	1398	1386	1003	975
3900	3818	1613	1641	1787	1756
1905	1854	1479	1503	857	883
7872	7718	1540	1503	1974	1945
1174	1155	520	<800	1707	1631
7015	7139	219	<800	3835	3756
2852	2868	1571	1503	6586	6551
221	<800	154	<800	178	<800
1002	1055	5077	5136	2905	2871
201	<800	2156	2190	2500	2501
6717	6864	1075	1089	389	<800
237	<800	162	<800	41	<800
2737	2749	2752	2834	685	<800
3448	3416	1647	1641	2598	2662
3256	3238	7059	7056	248	<800
5801	5759	1547	1503	2152	2210
1512	1497	5163	5136	431	<800
1398	1392	8679	8719	237	<800
8413	8333	2033	2035	3380	3411
6621	6614	886	892	5694	5744
645	<800	---	3255	3255	3265
1026	1055	---	183	183	<800
14333	14484	---	3128	3128	3144
---	---	---	10701	10701	10790
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Query Match 100.0%; Score 51; DB 9; Length 177334;  
Best Local Similarity 100.0%; Pred.No. 1.6e-19;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACACTGGTCTTCTGCTTATCCGGGCAAGAACTTATCGAAATACA 51

DB 65693 GGTACCACTGGTCTTCTGCTTATCCGGGCAAGAACTTATCGAAATACA 65743

RESULT 9  
AC104439  
LOCUS  
DEFINITION  
AC104439 AC024739  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
AUTHORS  
1 (bases 1 to 197279)  
Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,  
Saenphimmachak,C., Phelps,K.A., Buckley,D., Kibukawa,M., Raymond,C.  
and Haugen,B.D.  
Direct Submission  
Unpublished  
2 (bases 1 to 197279)  
Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,B.D.  
Direct Submission  
Submitted (11-DEC-2001) Genome Center, University of Washington,  
Box 352145, Seattle, WA 98195, USA  
3 (bases 1 to 197279)  
Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,  
Saenphimmachak,C., Phelps,K.A., Buckley,D., Kibukawa,M., Raymond,C.  
and Haugen,B.D.  
Direct Submission  
Submitted (20-JUN-2002) Genome Center, University of Washington,  
Box 352145, Seattle, WA 98195, USA  
On Jun 20, 2002 this sequence version replaced gi:17488621.  
----- Genome Center  
Center: University of Washington Genome Center  
Center Code: UWGC  
Web site: http://www.genome.washington.edu  
Contact: uwgctg@u.washington.edu  
Drafting Center: WUGSC  
----- Project Information  
Center project name: Chr-3  
Center clone name: RP11-793E15 (bc0564)  
----- Summary Statistics  
Sequencing vector: unknown; 52% of reads  
Sequencing method: plasmid; 108752; 48% of reads  
Chemistry: Dye-terminator ET; 94% of reads  
Chemistry: Dye-terminator Big Dye; 6% of reads  
Assembly program: Phrap; version 0.990319  
Consensus quality: 197168 bases at least Q40  
Consensus quality: 197255 bases at least Q30  
Consensus quality: 197275 bases at least Q20  
Insert size: 197279; sum-of-contigs  
Quality coverage: 8.2x in Q20 bases; sum-of-contigs  
-----  
Overlapping Sequences:  
5': RP11-51E8 (UWGC:bc0216) AC026349  
3': CTD-2563A18 (UWGC:bc0730)  
-----  
Sequence Quality Assessment:  
This entry has been annotated with sequence quality  
estimates computed by the Phrap assembly program.  
All manually edited bases have been reduced to quality zero.  
Quality levels above 40 are expected to have less than  
1 error in 10,000 bp.  
Base-by-base quality values are not generally visible from the  
Genbank flat file format but are available as part  
of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted:  
all regions were either double-stranded or sequenced with an  
alternate chemistry or covered by high quality data (i.e., Phred  
quality >= 30); an attempt was made to resolve all sequencing  
problems, such as compressions and repeats; all regions were  
covered by at least one plasmid subclone or more than one M13

subclone; and the assembly was confirmed by restriction digest.

#### Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

HindIII				BglII				EcoRI			
SeqDerMap	FngPrnt	SeqDerMap	FngPrnt	SeqDerMap	FngPrnt	SeqDerMap	FngPrnt	SeqDerMap	FngPrnt	SeqDerMap	FngPrnt
2687	2617	8949	8586	8996	8661	8996	8661	8996	8661	8996	8661
6382	6410	2067	2160	6	<800	6	<800	6	<800	6	<800
512	<800	7846	7940	2742	2803	2742	2803	2742	2803	2742	2803
449	<800	3734	3895	5376	5324	5376	5324	5376	5324	5376	5324
2602	2763	1334	1301	1493	1478	1493	1478	1493	1478	1493	1478
2590	2617	2287	2309	823	835	823	835	823	835	823	835
8313	8291	1814	1918	1962	2002	1962	2002	1962	2002	1962	2002
1711	1683	691	<800	2900	2954	2900	2954	2900	2954	2900	2954
9821	9472	5477	5348	1484	1478	1484	1478	1484	1478	1484	1478
516	<800	305	<800	1005	995	1005	995	1005	995	1005	995
8587	8291	25245	25541	1181	1171	1181	1171	1181	1171	1181	1171
7446	7581	3988	4121	18560	19002	18560	19002	18560	19002	18560	19002
2088	2075	1633	1598	3603	3579	3603	3579	3603	3579	3603	3579
2509	2617	631	<800	4943	5076	4943	5076	4943	5076	4943	5076
3519	3501	90	<800	3239	3241	3239	3241	3239	3241	3239	3241
26	<800	402	<800	953	995	953	995	953	995	953	995
925	933	3350	3490	1621	1615	1621	1615	1621	1615	1621	1615
98	<800	4577	4515	6827	6900	6827	6900	6827	6900	6827	6900
6409	6410	1229	1183	79	<800	79	<800	79	<800	79	<800
1383	1376	4221	4331	16418	16263	16418	16263	16418	16263	16418	16263
16048	15829	3980	4121	3361	3241	3361	3241	3361	3241	3361	3241
1876	1877	2548	2497	872	881	872	881	872	881	872	881
4169	4068	674	<800	4220	4193	4220	4193	4220	4193	4220	4193
1674	1683	2332	2309	2848	2803	2848	2803	2848	2803	2848	2803
52	<800	11445	11045	2283	2318	2283	2318	2283	2318	2283	2318
5227	5082	5692	5632	3211	3241	3211	3241	3211	3241	3211	3241
15464	15829	1385	1414	4615	4632	4615	4632	4615	4632	4615	4632

14333	14296	608	<800	6823	6900
1026	1026	3930	3895	886	881
645	<800	1465	1414	2032	2002
6621	6410	2382	2497	8680	8661
8413	8291	747	<800	5163	5076
1401	1376	1951	2012	1547	1478
1512	1471	642	<800	7058	6900
5801	5644	21060	21003	1647	1615
3256	3278	3700	3666	2753	2803
3448	3501	1321	1301	162	<800
2738	2763	10705	10502	1078	1093
237	<800	3128	3317	2156	2173
6715	6823	183	<800	5077	5076
201	<800	3255	3490	154	<800
1002	1026	5693	5632	1571	1478
221	<800	3380	3317	219	<800
2854	2899	237	<800	520	<800
6998	7317	431	<800	1540	1478
1174	1145	2152	2160	1479	1478
7876	8291	249	<800	1613	1615
1911	1877	2599	2778	1399	1478
3899	3847	685	<800	9553	9383
5672	5644	41	<800	166	<800
1711	1683	388	<800	13615	13115
862	854	2500	2497	4731	4632
2368	2389	2889	2778	5159	5076
		178	<800	4503	4430
		6589	6728	6607	6900
		3836	3895	2766	2803

Query Match 100.0%; Score 51; DB 9; Length 197279;  
Best Local Similarity 100.0%; Pred. No. 1.6e-19;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACCACTGGTCTTCTTGCTTATCCGGCAAGAACTTATCGAATACA 51  
Db 167486 GGTACCACTGGTCTTCTTGCTTATCCGGCAAGAACTTATCGAATACA 167536

#### RESULT 10

HSA312688

LOCUS

DEFINITION

SEQUENCING IN PROGRESS \*\*\*

220965 bp DNA linear

HTG 15-MAY-2002

3 clone RP6-3923 map 3p21.3, \*\*\*

26 ordered pieces.

ACCESSION AJ312688  
VERSION AJ312688.2 GI:13559235  
KEYWORDS HTG; HTGS\_PHASE2.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Kiss, H., Yang, Y., Kiss, C., Andersson, K., Klein, G., Inreh, S. and  
Dumanski, J.P.  
TITLE The transcriptional map of the common eliminated region 1 (C3CER1)  
in 3p21.3  
JOURNAL Eur. J. Hum. Genet. 10 (1), 52-61 (2002)  
MEDLINE 21906202  
PUBMED 11896456  
REFERENCE 2 (bases 1 to 220965)  
AUTHORS Kiss, H.  
TITLE Direct Submission  
JOURNAL Submitted (01-APR-2001) Kiss H., Microbiology and Tumorbiology  
Center (MTC), Karolinska Institute, Box 280, Stockholm, S-17177,  
SWEDEN  
COMMENT On Apr 5, 2001 this sequence version replaced gi:13548633.  
The sequence is a consensus sequence of clone RP4-787c23 (1-140400  
bp),  
clone RP6-32g23 (31212-220965 bp), clone RP6-146el (partially,  
1-6800 bp)  
and clone RP6-188g11 (partially, 1-108303 bp). The sequencing  
contigs are  
in order and the gaps between them are represented by 100 Ns.  
Contig 1:  
1-11731 bp Contig 2: 11832-26218 bp Contig 3: 26319-28347 bp  
Contig 4:  
28448-42160 bp Contig 5: 42261-55059 bp Contig 6: 55160-61578 bp  
Contig  
7: 61679-97342 bp Contig 8: 97443-117655 bp Contig 9:  
117756-118727 bp  
Contig 10: 118828-121834 bp Contig 11: 121935-127855 bp Contig  
12:  
127956-129383 bp Contig 13: 129484-131747 bp Contig 14:  
131848-132316 bp  
Contig 15: 132417-134455 bp Contig 16: 134556-135527 bp Contig  
17:  
135628-189051 bp Contig 18: 189152-189476 bp Contig 19:  
189577-191375 bp  
Contig 20: 191476-201473 bp Contig 21: 201574-202307 bp Contig  
22:  
202408-204878 bp Contig 23: 204979-213531 bp Contig 24:  
213632-218109 bp  
Contig 25: 218210-219800 bp Contig 26: 219901-220965 bp.  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 26 contigs. Gaps between the contigs  
\* are represented as runs of N. The order of the pieces  
\* is believed to be correct as given, however the sizes  
\* of the gaps between them are based on estimates that have  
\* provided by the submitter.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.  
\* 1 11731: contig of 11731 bp in length  
\* 11732 11831: gap of 100 bp  
\* 11832 26218: contig of 14387 bp in length  
\* 26219 26318: gap of 100 bp  
\* 26319 28347: contig of 2029 bp in length  
\* 28348 42160: gap of 100 bp  
\* 42161 42360: contig of 13713 bp in length  
\* 42361 55059: contig of 200 bp  
\* 55060 55159: contig of 12699 bp in length  
\* 55160 61578: gap of 100 bp  
\* 61579 61578: contig of 6419 bp in length  
\* 61679 97342: contig of 35664 bp in length  
\* 97343 97442: gap of 100 bp  
\* 97443 117655: contig of 20213 bp in length

117556 117755: gap of 100 bp  
117756 118727: contig of 972 bp in length  
118728 118827: gap of 100 bp  
118828 121834: contig of 3007 bp in length  
121835 121934: gap of 100 bp  
121935 127855: contig of 5921 bp in length  
127856 127955: gap of 100 bp  
127956 129383: contig of 1428 bp in length  
129384 129483: gap of 100 bp  
129484 131747: contig of 2264 bp in length  
131748 131847: gap of 100 bp  
131848 132316: contig of 469 bp in length  
132317 132416: gap of 100 bp  
132417 134455: contig of 2039 bp in length  
134456 134555: gap of 100 bp  
134556 135527: contig of 972 bp in length  
135528 135627: gap of 100 bp  
135628 189051: contig of 53424 bp in length  
189052 189151: gap of 100 bp  
189152 189476: contig of 325 bp in length  
189477 189576: gap of 100 bp  
189577 191375: contig of 1799 bp in length  
191376 191475: gap of 100 bp  
191476 201473: contig of 9998 bp in length  
201474 201573: gap of 100 bp  
201574 202307: contig of 734 bp in length  
202308 202407: gap of 100 bp  
202408 204878: contig of 2471 bp in length  
204879 204979: gap of 100 bp  
204979 213531: contig of 8553 bp in length  
213532 213631: gap of 100 bp  
213632 218109: contig of 4478 bp in length  
218110 218209: gap of 100 bp  
218210 219800: contig of 1591 bp in length  
219801 219900: gap of 100 bp  
219901 220965: contig of 1065 bp in length.

FEATURES  
source

1. 220965  
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/chromosome="3"  
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/clone="RP6-32g23"

ORIGIN

Query Match 100.0%; Score 51; DB 2; Length 220965;  
Best Local Similarity 100.0%; Pred No. 1.6e-19; Mismatches 0; Indels 0; Gaps 0;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGTACCACTGGTCTTCTTGCTTATCCGGGCAAGAACTTATCGAAATACA 51  
Db 121110 GGTACCACTGGTCTTCTTGCTTATCCGGGCAAGAACTTATCGAAATACA 121160

RESULT 11

AF224495 260 bp mRNA linear PRI 02-MAY-2001  
LOCUS Homo sapiens CC chemokine receptor 3 (CCR3) mRNA, partial cds.  
DEFINITION Homo sapiens CC chemokine receptor 3 (CCR3) mRNA, partial cds.  
ACCESSION AF224495  
VERSION AF224495.1 GI:139244481  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 260)  
AUTHORS Scotet, E.J.  
TITLE CCR3 expression is associated with chromatin remodeling in Th2 cells  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 260)  
AUTHORS Scotet, E.J.

TITLE Direct Submission  
JOURNAL Submitted (13-JAN-2000) Basel Institute for Immunology, 487  
Grenzacherstrasse, Basel CH-4005, Switzerland

## FEATURES

source Location/Qualifiers

1..260  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
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## gene

1..>260  
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## CDS

91..>260  
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/product="CC chemokine receptor 3"  
/protein\_id="AAK49027.1"  
/db\_xref="GI:13924482"  
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FTVGLLGNVVVV"

## ORIGIN

Query Match 94.1%; Score 48; DB 9; Length 260;  
Best Local Similarity 100.0%; Pred. No. 1.2e-17;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ACCACTGGTCTTCTTGCTTATCCGGGCAAGAACTTATCGAATACA 51

Db 1 ACCACTGGTCTTCTTGCTTATCCGGGCAAGAACTTATCGAATACA 48

## RESULT 12

AF262301 AF262301 406 bp mRNA linear PRI 26-JUN-2002  
LOCUS Homo sapiens clone 4 CC chemokine receptor 3 (CCR3) mRNA, partial  
cds.

ACCESSION AF262301 GI:19171644

## KEYWORDS

AF262301.1 Homo sapiens (human)

## SOURCE

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 406)  
Vijh,S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and  
Michael,N.L.

Transcription Regulation of Human Chemokine Receptor CCR3: Evidence  
for a Rare TATA-less Promoter Structure Conserved Between

JOURNAL Genomics 80 (1), 86-95 (2002)

MEDLINE 22074933

PUBMED 12079287

REFERENCE 2 (bases 1 to 406)

Vijh,S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.

Direct Submission

Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis,

Walter Reed Army Institute of Research, 1600 E. Gude Drive,

Rockville, MD 20850, USA

Location/Qualifiers

1..406  
/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/chromosome="3"

/map="3p21"

/clone="4"

1..>406  
/gene="CCR3"

160..>406  
/gene="CCR3"

/notes="G-protein coupled receptor; principal eotaxin

receptor expressed on eosinophils, CD4 Th2 lymphocytes,

CD8 lymphocytes, microglia, dendritic cells, and

monocytes"

/codon\_start=1

/product="CC chemokine receptor 3"

/protein\_id="AAL85630.1"

/db\_xref="GI:19171645"

/translation="MTSLDTVETFGTTSYDDVGLLCEKADTRALMAQFVPPLYSLV

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## ORIGIN

Query Match 94.1%; Score 48; DB 9; Length 406;  
Best Local Similarity 100.0%; Pred. No. 1.2e-17;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ACCACTGGTCTTCTTGCTTATCCGGGCAAGAACTTATCGAATACA 51

Db 1 ACCACTGGTCTTCTTGCTTATCCGGGCAAGAACTTATCGAATACA 48

## RESULT 13

AF262302 AF262302 410 bp mRNA linear PRI 26-JUN-2002  
LOCUS Homo sapiens clone 5 CC chemokine receptor 3 (CCR3) mRNA, partial  
cds.

ACCESSION AF262302

VERSION AF262302.1 GI:19171646

## KEYWORDS

AF262302.1 Homo sapiens (human)

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 410)  
Vijh,S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and  
Michael,N.L.

Transcription Regulation of Human Chemokine Receptor CCR3: Evidence  
for a Rare TATA-less Promoter Structure Conserved Between

JOURNAL Genomics 80 (1), 86-95 (2002)

MEDLINE 22074933

PUBMED 12079287

REFERENCE 2 (bases 1 to 410)

Vijh,S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.

Direct Submission

Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis,

Walter Reed Army Institute of Research, 1600 E. Gude Drive,

Rockville, MD 20850, USA

Location/Qualifiers

1..410  
/organism="Homo sapiens"

/mol\_type="mRNA"

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/chromosome="3"

/map="3p21"

/clone="5"

/cell\_type="primary eosinophil"

1..>410  
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170..>410  
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/note="G-protein coupled receptor; principal eotaxin

receptor expressed on eosinophils, CD4 Th2 lymphocytes,

CD8 lymphocytes, microglia, dendritic cells, and

monocytes"

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/product="CC chemokine receptor 3"

/protein\_id="AAL85631.1"

/db\_xref="GI:19171647"

/translation="MTSLDTVETFGTTSYDDVGLLCEKADTRALMAQFVPPLYSLV

FTVGLLGNVVVVVILIKYRRLRMNTNIIYLLNLAISD"

## ORIGIN

Query Match 94.1%; Score 48; DB 9; Length 410;  
Best Local Similarity 100.0%; Pred. No. 1.2e-17;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 4 ACCACTGGTCTTCTTGCTTATCCGGGCAAGAACTTATCGAATACA 51
Db 1 ACCACTGGTCTTCTTGCTTATCCGGGCAAGAACTTATCGAATACA 48

RESULT 14
AF262303 212 bp mRNA linear PRI 26-JUN-2002
LOCUS Homo sapiens clone 6 CC chemokine receptor 3 (CCR3) mRNA, partial
DEFINITION Cds.
ACCESSION AF262303
VERSION AF262303.1 GI:19171648
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 212)
AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and
Michael,N.L.
TITLE Transcription Regulation of Human Chemokine Receptor CCR3: Evidence
for a Rare TATA-less Promoter Structure Conserved between
Drosophila and Humans
JOURNAL Genomics 80 (1), 86-95 (2002)
MEDLINE 22074933
PUBMED 12079287
REFERENCE 2 (bases 1 to 212)
AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.
TITLE Direct Submission
JOURNAL Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis,
Walter Reed Army Institute of Research, 1600 E. Gude Drive,
Rockville, MD 20850, USA
FEATURES
source
Location/Qualifiers
1..212
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/map="3p21"
/chromosome="3"
/clone="6"
1..>212
/gene="CCR3"
150..>212
/gene="CCR3"
/note="G-protein coupled receptor; principal eotaxin
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CD8 lymphocytes, microglia, dendritic cells, and
monocytes"
/codon_start=1
/product="CC chemokine receptor 3"
/protein_id="AA05632.1"
/db_xref="GI:19171649"
/translation="MTTSLDTVETFGTTSYYDDVG"

ORIGIN
Query Match 92.2%; Score 47; DB 9; Length 212;
Best Local Similarity 100.0%; Pred.No. 4.8e-17;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCACCTGGTCTTCTTGCTTATCCGGGCAAGAACTTATCGAATACA 51
Db 1 CCACCTGGTCTTCTTGCTTATCCGGGCAAGAACTTATCGAATACA 47

RESULT 15
AF262304 436 bp mRNA linear PRI 26-JUN-2002
LOCUS Homo sapiens clone 7 CC chemokine receptor 3-like mRNA, partial
DEFINITION sequence, alternatively spliced.
ACCESSION AF262304
VERSION AF262304.1 GI:19171650
KEYWORDS
SOURCE Homo sapiens (human)
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 436)
AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and
Michael,N.L.
TITLE Transcription Regulation of Human Chemokine Receptor CCR3: Evidence
for a Rare TATA-less Promoter Structure Conserved between
Drosophila and Humans
JOURNAL Genomics 80 (1), 86-95 (2002)
MEDLINE 22074933
PUBMED 12079287
REFERENCE 2 (bases 1 to 436)
AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.
TITLE Direct Submission
JOURNAL Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis,
Walter Reed Army Institute of Research, 1600 E. Gude Drive,
Rockville, MD 20850, USA
FEATURES
source
Location/Qualifiers
1..436
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="3"
/map="3p21"
/clone="7"
1..436
/cell_type="primary eosinophil"
misc_feature 1..436
/notes="CC chemokine receptor 3-like; contains exon 1, exon
3, and intron 3 of the CCR3 gene; alternatively spliced"

ORIGIN
Query Match 92.2%; Score 47; DB 9; Length 436;
Best Local Similarity 100.0%; Pred.No. 4.7e-17;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCACCTGGTCTTCTTGCTTATCCGGGCAAGAACTTATCGAATACA 51
Db 1 CCACCTGGTCTTCTTGCTTATCCGGGCAAGAACTTATCGAATACA 47

Search completed: August 2, 2004, 19:07:50
Job time : 1146.66 secs
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**This Page Blank (uspto)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 2, 2004, 19:08:00 ; Search time 258.078 Seconds  
(without alignments)  
968.934 Million cell updates/sec

Title: US-10-068-067-16.

Perfect score: 51  
Sequence: 1 ggtaccactggtctcttgtt.....caagaacttatcgaaataca 51

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 3222919 seqs, 2451570024 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6445838

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA:

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- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq\*
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- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq\*
- 13: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq\*
- 17: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq\*
- 18: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq\*
- 19: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	51	100.0	51	14	US-10-068-067-16	Sequence 15, Appl
2	51	100.0	51	14	US-10-068-067-21	Sequence 21, Appl
3	51	100.0	2895	14	US-10-068-067-11	Sequence 11, Appl
4	35	68.6	1193	15	US-10-283-028-3	Sequence 3, Appl
5	22	43.1	22	14	US-10-068-067-17	Sequence 17, Appl
6	22	43.1	22	14	US-10-068-067-18	Sequence 18, Appl
7	22	43.1	22	14	US-10-068-067-23	Sequence 23, Appl
8	21	41.2	21	14	US-10-068-067-19	Sequence 19, Appl
9	21	41.2	21	14	US-10-068-067-22	Sequence 22, Appl
10	21	41.2	21	14	US-10-068-067-24	Sequence 24, Appl
c 11	17	33.3	11124	14	US-10-108-605-286	Sequence 286, App
c 12	17	33.3	11184	14	US-10-108-605-284	Sequence 284, App
c 13	16	31.4	21	16	US-10-349-143-9067	Sequence 9067, App
c 14	16	31.4	265	9	US-09-983-965-904	Sequence 904, App

15	31.4	465	17	US-10-437-963-67946	Sequence 67946, A
c 16	31.4	586	9	US-09-864-761-12607	Sequence 12607, A
c 17	31.4	1179	17	US-10-437-963-57307	Sequence 57307, A
c 18	31.4	1251	15	US-10-198-846-13243	Sequence 13243, A
c 19	31.4	1761	17	US-10-437-963-67947	Sequence 67947, A
c 20	31.4	1967	17	US-10-437-963-23487	Sequence 23487, A
21	31.4	3153	13	US-10-282-122A-41935	Sequence 41935, A
22	31.4	3153	13	US-09-796-692-2584	Sequence 2584, App
23	29.4	234	15	US-10-040-862-2584	Sequence 2584, App
24	29.4	234	16	US-10-057-475B-2584	Sequence 2584, App
25	29.4	234	16	US-10-154-894B-2584	Sequence 2584, App
26	29.4	407	10	US-09-814-353-18713	Sequence 18713, A
27	29.4	423	10	US-09-814-353-21865	Sequence 21865, A
28	29.4	489	9	US-09-070-927A-977	Sequence 977, App
29	29.4	537	10	US-09-991-936-1052	Sequence 1052, App
30	29.4	695	13	US-10-027-632-114054	Sequence 114054, A
31	29.4	695	13	US-10-027-632-114055	Sequence 114055, A
32	29.4	695	13	US-10-027-632-114056	Sequence 114056, A
33	29.4	695	16	US-10-027-632-114054	Sequence 114054, A
34	29.4	695	16	US-10-027-632-114055	Sequence 114055, A
35	29.4	695	16	US-10-027-632-114056	Sequence 114056, A
c 36	29.4	731	13	US-10-027-632-173383	Sequence 173383, A
c 37	29.4	731	16	US-10-027-632-173383	Sequence 173383, A
c 38	29.4	767	13	US-10-027-632-14404	Sequence 14404, A
c 39	29.4	767	13	US-10-027-632-145338	Sequence 145338, A
c 40	29.4	767	13	US-10-027-632-145339	Sequence 145339, A
c 41	29.4	767	13	US-10-027-632-145340	Sequence 145340, A
c 42	29.4	767	16	US-10-027-632-14404	Sequence 14404, A
c 43	29.4	767	16	US-10-027-632-145338	Sequence 145338, A
c 44	29.4	767	16	US-10-027-632-145339	Sequence 145339, A
c 45	29.4	767	16	US-10-027-632-145340	Sequence 145340, A

ALIGNMENTS

RESULT 1  
US-10-068-067-16  
; Sequence 16, Application US/10068067  
; Publication No. US20020151064A1  
; GENERAL INFORMATION:  
; APPLICANT: Rothenberg, Marc E.  
; APPLICANT: Zimmermann, Nives  
; APPLICANT: Children's Hospital Medical Center  
; TITLE OF INVENTION: REGULATION OF CCR3 EXPRESSION  
; FILE REFERENCE: CMC-153  
; CURRENT APPLICATION NUMBER: US/10/068,067  
; CURRENT FILING DATE: 2002-02-05  
; PRIOR APPLICATION NUMBER: 60/267,073  
; PRIOR FILING DATE: 2001-02-07  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 16  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-068-067-16

Query Match 100.0%; Score 51; DB 14; Length 51;  
Best Local Similarity 100.0%; Pred No. 2.2e-20;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGTACCACCTGGTCTTCTTGTGCTTATCCGGGCAAGAACTTATCGAAATACA 51  
Db 1 GGTACCACCTGGTCTTCTTGTGCTTATCCGGGCAAGAACTTATCGAAATACA 51  
RESULT 2  
US-10-068-067-21  
; Sequence 21, Application US/10068067  
; Publication No. US20020151064A1  
; GENERAL INFORMATION:  
; APPLICANT: Rothenberg, Marc E.

APPLICANT: Zimmermann, Nives  
APPLICANT: Children's Hospital Medical Center  
TITLE OF INVENTION: REGULATION OF CCR3 EXPRESSION  
FILE REFERENCE: CMC-153  
CURRENT FILING DATE: 2002-02-05  
PRIORITY FILING DATE: 2002-02-05  
PRIORITY FILING DATE: 2001-02-07  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 21  
LENGTH: 51  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-10-068-067-21

Query Match 100.0%; Score 51; DB 14; Length 51;  
Best Local Similarity 70.6%; Pred. No. 2.2e-20;  
Matches 36; Conservative 15; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACCACTGGTCTTCTTGCTTATCCGGGCAAGAACTTATCGAAATACA 51  
DB 1 GGUACCACUGGCUUCUUGGCUUAUCCGGGCAAGAACTTATCGAAATACA 51

RESULT 3  
US-10-068-067-11  
Sequence 11, Application US/10068067  
Publication No. US20020151064A1  
GENERAL INFORMATION:  
APPLICANT: Rothenberg, Marc E.  
APPLICANT: Zimmermann, Nives  
APPLICANT: Children's Hospital Medical Center  
TITLE OF INVENTION: REGULATION OF CCR3 EXPRESSION  
FILE REFERENCE: CMC-153  
CURRENT APPLICATION NUMBER: US/10/068,067  
CURRENT FILING DATE: 2002-02-05  
PRIORITY FILING DATE: 2002-02-05  
PRIORITY FILING DATE: 2001-02-07  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 11  
LENGTH: 2895  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-068-067-11

Query Match 100.0%; Score 51; DB 14; Length 2895;  
Best Local Similarity 100.0%; Pred. No. 2.5e-20;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACCACTGGTCTTCTTGCTTATCCGGGCAAGAACTTATCGAAATACA 51  
DB 1561 GGTACCACTGGTCTTCTTGCTTATCCGGGCAAGAACTTATCGAAATACA 1611

RESULT 4  
US-10-283-028-3  
Sequence 3, Application US/10283028  
Publication No. US20030143684A1  
GENERAL INFORMATION:  
APPLICANT: Gerard, Craig J.  
Gerard, No. US20030143684A1 p. 1  
Mackay, Charles R.  
Ponath, Paul D.  
Qin, Shixin  
Post, Theodore W.  
TITLE OF INVENTION: G PROTEIN-COUPLED RECEPTOR GENE CCR3 AND ANTAGONISTS THEREOF  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive

CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/283,028  
FILING DATE: 28-Oct-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/720,565  
FILING DATE: 30-SEP-1996  
APPLICATION NUMBER: PCT/US96/00608  
FILING DATE: 19-JAN-1996  
APPLICATION NUMBER: US 08/375,199  
FILING DATE: 19-JAN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Brook, David E.  
REGISTRATION NUMBER: 22,592  
REFERENCE/DOCKET NUMBER: LKS94-05A2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1193 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 92..1156  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-10-283-028-3

Query Match 68.6%; Score 35; DB 15; Length 1193;  
Best Local Similarity 100.0%; Pred. No. 8.9e-11;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TTGTGCTTATCCGGGCAAGAACTTATCGAAATACA 51  
DB 1 TTGTGCTTATCCGGGCAAGAACTTATCGAAATACA 35

RESULT 5  
US-10-068-067-17  
Sequence 17, Application US/10068067  
Publication No. US20020151064A1  
GENERAL INFORMATION:  
APPLICANT: Rothenberg, Marc E.  
APPLICANT: Zimmermann, Nives  
APPLICANT: Children's Hospital Medical Center  
TITLE OF INVENTION: REGULATION OF CCR3 EXPRESSION  
FILE REFERENCE: CMC-153  
CURRENT APPLICATION NUMBER: US/10/068,067  
CURRENT FILING DATE: 2002-02-05  
PRIORITY FILING DATE: 2001-02-07  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 17  
LENGTH: 22  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-068-067-17

Query Match 43.1%; Score 22; DB 14; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.0046;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACCACTGGTCTTCTGTGC 22  
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 DB 1 GGTACCACTGGTCTTCTGTGC 22

## RESULT 6

US-10-068-067-18  
 ; Sequence 18, Application US/10068067  
 ; Publication No. US20020151064A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rothenberg, Marc E.  
 ; APPLICANT: Zimmermann, Nives  
 ; APPLICANT: Children's Hospital Medical Center  
 ; TITLE OF INVENTION: REGULATION OF CCR3 EXPRESSION  
 ; FILE REFERENCE: CMC-153  
 ; CURRENT APPLICATION NUMBER: US/10/068,067  
 ; CURRENT FILING DATE: 2002-02-05  
 ; PRIOR APPLICATION NUMBER: 60/267,073  
 ; PRIOR FILING DATE: 2001-02-07  
 ; NUMBER OF SEQ ID NOS: 24  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 18  
 ; LENGTH: 22  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-068-067-18

Query Match 43.1%; Score 22; DB 14; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 0.0046;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CTTGTGCTTATCCGGGCAAGAA 37  
 |||||  
 DB 1 CTTGTGCTTATCCGGGCAAGAA 22

## RESULT 7

US-10-068-067-23  
 ; Sequence 23, Application US/10068067  
 ; Publication No. US20020151064A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rothenberg, Marc E.  
 ; APPLICANT: Zimmermann, Nives  
 ; APPLICANT: Children's Hospital Medical Center  
 ; TITLE OF INVENTION: REGULATION OF CCR3 EXPRESSION  
 ; FILE REFERENCE: CMC-153  
 ; CURRENT APPLICATION NUMBER: US/10/068,067  
 ; CURRENT FILING DATE: 2002-02-05  
 ; PRIOR APPLICATION NUMBER: 60/267,073  
 ; PRIOR FILING DATE: 2001-02-07  
 ; NUMBER OF SEQ ID NOS: 24  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 23  
 ; LENGTH: 22  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens  
 US-10-068-067-23

Query Match 43.1%; Score 22; DB 14; Length 22;  
 Best Local Similarity 72.7%; Pred. No. 0.0046;  
 Matches 16; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 16 CTTGTGCTTATCCGGGCAAGAA 37  
 |||||  
 DB 1 CUUGGCUUACUGGGCAAGAA 22

## RESULT 8

US-10-068-067-19  
 ; Sequence 19, Application US/10068067  
 ; Publication No. US20020151064A1

; GENERAL INFORMATION:  
 ; APPLICANT: Rothenberg, Marc E.  
 ; APPLICANT: Zimmermann, Nives  
 ; APPLICANT: Children's Hospital Medical Center  
 ; TITLE OF INVENTION: REGULATION OF CCR3 EXPRESSION  
 ; FILE REFERENCE: CMC-153  
 ; CURRENT APPLICATION NUMBER: US/10/068,067  
 ; CURRENT FILING DATE: 2002-02-05  
 ; PRIOR APPLICATION NUMBER: 60/267,073  
 ; PRIOR FILING DATE: 2001-02-07  
 ; NUMBER OF SEQ ID NOS: 24  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 19  
 ; LENGTH: 21  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-068-067-19

Query Match 41.2%; Score 21; DB 14; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 0.018;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 GCAAGACTTATCGAAATACA 51  
 |||||  
 DB 1 GCAAGACTTATCGAAATACA 21

## RESULT 9

US-10-068-067-22  
 ; Sequence 22, Application US/10068067  
 ; Publication No. US20020151064A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rothenberg, Marc E.  
 ; APPLICANT: Zimmermann, Nives  
 ; APPLICANT: Children's Hospital Medical Center  
 ; TITLE OF INVENTION: REGULATION OF CCR3 EXPRESSION  
 ; FILE REFERENCE: CMC-153  
 ; CURRENT APPLICATION NUMBER: US/10/068,067  
 ; CURRENT FILING DATE: 2002-02-05  
 ; PRIOR APPLICATION NUMBER: 60/267,073  
 ; PRIOR FILING DATE: 2001-02-07  
 ; NUMBER OF SEQ ID NOS: 24  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 22  
 ; LENGTH: 21  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens  
 US-10-068-067-22

Query Match 41.2%; Score 21; DB 14; Length 21;  
 Best Local Similarity 61.9%; Pred. No. 0.018;  
 Matches 13; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACCACTGGTCTTCTGTGC 21  
 |||||  
 DB 1 GGUACCACUGGCUUCUUGUG 21

## RESULT 10

US-10-068-067-24  
 ; Sequence 24, Application US/10068067  
 ; Publication No. US20020151064A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rothenberg, Marc E.  
 ; APPLICANT: Zimmermann, Nives  
 ; APPLICANT: Children's Hospital Medical Center  
 ; TITLE OF INVENTION: REGULATION OF CCR3 EXPRESSION  
 ; FILE REFERENCE: CMC-153  
 ; CURRENT APPLICATION NUMBER: US/10/068,067  
 ; CURRENT FILING DATE: 2002-02-05  
 ; PRIOR APPLICATION NUMBER: 60/267,073  
 ; PRIOR FILING DATE: 2001-02-07  
 ; NUMBER OF SEQ ID NOS: 24

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-068-067-24

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Query Match 41.2%; Score 21; DB 14; Length 21;  
Best Local Similarity 81.0%; Pred. No. 0.018;  
Matches 17; Conservative 4; Mismatches 0; Indels

QY 31 GCAAGAACTTATCGAAATACA 51  
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Db 1 GCAAGAACUUAUCGAAAUACA 21

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RESULT 11
US-10-108-605-286/c
/ Sequence 286, Application US/10108605
/ Publication No. US20020160934A1
/ GENERAL INFORMATION:
/ APPLICANT: Broad, Julie
/ APPLICANT: Stam, Lynn
/ APPLICANT: Bachmann, Jane
/ APPLICANT: Kamdar, Kim
/ TITLE OF INVENTION: NUCLEIC ACID SEQUENCES
/ TITLE OF INVENTION: PROTEINS ESSENTIAL FOR
/ FILE REFERENCES: 31133B
/ CURRENT APPLICATION NUMBER: US/10/108605
/ CURRENT FILING DATE: 2002-03-27
/ PRIOR APPLICATION NUMBER: US 09/761,144
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/176,444
/ PRIOR FILING DATE: 2000-01-14
/ NUMBER OF SEQ ID NOS: 361
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2866
/ LENGTH: 11124
/ TYPE: DNA
/ ORGANISM: Drosophila melanogaster
US-10-108-605-286

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Query Match      33.3%; Score 17; DB 14; Length 11124;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 33 AAGAACTTATCGAAATA 49  
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Db 3529 AAGAACTTATCGAAATA 3513

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RESULT 12
US/10-108-605-284/c
// Sequence 284, Application US/10108605
// Publication No. US20020160934A1
// GENERAL INFORMATION:
// APPLICANT: Broadam, Julie
// APPLICANT: Stam, Lynn
// APPLICANT: Bachmann, Jane
// APPLICANT: Kamdat, Kim
// TITLE OF INVENTION: NUCLEIC ACID SEQUENCE
// TITLE OF INVENTION: PROTEINS ESSENTIAL FOR
// FILE REFERENCE: 31133B
// CURRENT APPLICATION NUMBER: US/10/108,605
// CURRENT FILING DATE: 2002-03-27
// PRIOR APPLICATION NUMBER: US 09/761,142
// PRIOR FILING DATE: 2001-01-16
// PRIOR APPLICATION NUMBER: US 60/176,418
// PRIOR FILING DATE: 2000-01-14
// NUMBER OF SEQ IDS NOS: 361
// SOFTWARE: patentIn Ver. 2.1
// SEQ ID NO 284
// LENGTH: 11184

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; TYPE: DNA  
; ORGANISM: Drosophila melanogaster  
US-10-108-605-284

Query Match	33.3%	Score 17;	DB 14;	Length 11184;
Best Local Similarity	100.0%;	Pred. No. 5.5;		
Matches 17;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;

Qy 33 AAGAACTTATCGAAATA 49  
Db 3589 AAGAACTTATCGAAATA 3573

```

RESULT 13
US-10-349-143-9067
; Sequence 9067, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Il'ya
; TITLE OF INVENTION: Biallelic markers
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/10/349
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,9
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APP
; PRIOR FILING DATE: EARLIER FILING DAT
; PRIOR APPLICATION NUMBER: EARLIER APP
; PRIOR FILING DATE: EARLIER FILING DAT
; PRIOR APPLICATION NUMBER: EARLIER APP
; PRIOR FILING DATE: EARLIER FILING DAT
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 9067
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..21
; OTHER INFORMATION: downstream amplif
US-10-349-143-9067

```

Query Match	31.4%;	Score 16;	DB 16;	Length 21;
Best Local Similarity	100.0%;	Pred. No. 18;		
Matches 16:	Conservative	0;	Mismatches	0;
	Indels	0;	Gaps	0;

Qy 10 GGTCTTCTTGCTTA 25  
|||  
Db 1 GGTCTTCTTGCTTA 16

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RESULT 14
US-09-983-965-904/c
/ Sequence 904, Application US/09983965
/ Patent No. US20020137160A1
/ GENERAL INFORMATION:
/ APPLICANT: Warren, Wesley C.
/ APPLICANT: Tao, Nengbing C.
/ APPLICANT: Byatt, John C.
/ APPLICANT: Mathaleagan, Nagappan
/ TITLE OF INVENTION: NUCLEIC ACID AND
/ TITLE OF INVENTION: MUSCLE AND FAT
/ FILE REFERENCE: 37-21(10297)C
/ CURRENT APPLICATION NUMBER: US/09/98
/ CURRENT FILING DATE: 2001-10-26
/ PRIOR APPLICATION NUMBER: US 09/465,
/ PRIOR FILING DATE: 1999-12-15
/ PRIOR APPLICATION NUMBER: US 60/113,
/ PRIOR FILING DATE: 1998-12-17
/ NUMBER OF SEQ ID NOS: 5912
/ SEQ ID NO 904

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; LENGTH: 265
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; OTHER INFORMATION: Clone ID: 37-LIB188-012-Q1-E1-B2
US-09-983-965-904

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Query Match      31.4%; Score 16; DB 9; Length 265;
Best Local Similarity 100.0%; Pred.No. 19;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 16 CTTGTGCTTATCCGGG 31
    |||||
Db 217 CTTGTGCTTATCCGGG 202

```

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RESULT 15
US-10-437-963-67946
; Sequence 67946, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrew A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 67946
; LENGTH: 465
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_68757C.1
US-10-437-963-67946

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Query Match      31.4%; Score 16; DB 17; Length 465;
Best Local Similarity 100.0%; Pred.No. 20;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 32 CAAGAACTTATCGAAA 47
    |||||
Db 120 CAAGAACTTATCGAAA 135

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Search completed: August 2, 2004, 22:36:34
Job time : 259.078 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 2, 2004, 18:10:40 ; Search time 51.4397 Seconds  
(without alignments)  
550.208 Million cell updates/sec

Title: US-10-068-067-16

Perfect score: 51  
Sequence: 1 ggtaccactggctctctgtgt.....caagaacttatcgaaataca 51

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA:\*

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- 2: /cgm2\_6/ptodata/2/ina/5B\_COMB.seq:\*
- 3: /cgm2\_6/ptodata/2/ina/6A\_COMB.seq:\*
- 4: /cgm2\_6/ptodata/2/ina/6B\_COMB.seq:\*
- 5: /cgm2\_6/ptodata/2/ina/PTUS\_COMB.seq:\*
- 6: /cgm2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	68.6	1193	4	US-08-720-565-3
2	16	31.4	21	4	US-09-422-978-9067
3	16	31.4	698	4	US-09-634-238-126
4	15	29.4	2254	2	US-08-635-066-1
5	15	29.4	2787	4	US-09-134-000C-3185
6	15	29.4	3177	3	US-09-134-513-1
7	15	29.4	8920	2	US-08-446-855A-1
8	15	29.4	8920	3	US-09-150-741-1
9	15	29.4	11867	4	US-09-497-855A-32
10	14	27.5	281	4	US-08-469-260A-18
11	14	27.5	281	4	US-08-469-260A-20
12	14	27.5	281	4	US-08-488-446-18
13	14	27.5	281	4	US-08-488-446-20
14	14	27.5	281	4	US-08-467-344A-18
15	14	27.5	281	4	US-08-467-344A-20
16	14	27.5	435	4	US-09-489-039A-6593
17	14	27.5	462	4	US-09-621-976-15146
18	14	27.5	479	4	US-08-469-260A-25
19	14	27.5	479	4	US-08-469-260A-392
20	14	27.5	479	4	US-08-488-446-25
21	14	27.5	479	4	US-08-488-446-392
22	14	27.5	479	4	US-08-467-344A-25
23	14	27.5	479	4	US-08-467-344A-392
24	14	27.5	495	4	US-09-621-976-17953
25	14	27.5	508	4	US-09-621-976-9046
26	14	27.5	513	4	US-09-621-976-3690
27	14	27.5	517	4	US-09-621-976-1231

c	28	14	27.5	542	4	US-09-669-751-135	Sequence 135, App
c	29	14	27.5	678	4	US-09-543-681A-3526	Sequence 3526, App
c	30	14	27.5	865	4	US-09-640-419C-6	Sequence 6, Appli
c	31	14	27.5	1262	4	US-09-212-608B-29	Sequence 29, Appl
c	32	14	27.5	1262	4	US-09-064-411A-31	Sequence 31, Appl
c	33	14	27.5	1267	4	US-09-064-411A-22	Sequence 22, Appl
c	34	14	27.5	1267	4	US-09-280-428A-9	Sequence 9, Appli
c	35	14	27.5	1301	4	US-09-489-847-108	Sequence 108, App
c	36	14	27.5	1456	4	US-09-064-411A-23	Sequence 23, Appl
c	37	14	27.5	1578	4	US-09-252-991A-5039	Sequence 5039, Ap
c	38	14	27.5	1581	4	US-09-252-991A-5177	Sequence 5177, Ap
c	39	14	27.5	1760	4	US-09-495-050A-139	Sequence 139, App
c	40	14	27.5	2114	4	US-09-370-838-158	Sequence 158, App
c	41	14	27.5	2432	4	US-09-205-258-48	Sequence 48, Appl
c	42	14	27.5	2793	4	US-08-753-750B-1	Sequence 1, Appli
c	43	14	27.5	3142	1	US-08-110-158-3	Sequence 3, Appli
c	44	14	27.5	3142	4	US-09-023-655-1090	Sequence 1090, Ap
c	45	14	27.5	3144	5	PCT-US91-05059-1	Sequence 1, Appli

#### ALIGNMENTS

RESULT 1  
US-08-720-565-3  
; Sequence 3, Application US/08720565  
; Patent No. 6537764  
; GENERAL INFORMATION:  
; APPLICANT: Gerard, Craig J.  
; APPLICANT: Gerard, No. 6537764ma P.  
; APPLICANT: Mackay, Charles R.  
; APPLICANT: Ponath, Paul D.  
; APPLICANT: Post, Theodore W.  
; APPLICANT: Qin, Shixin  
; TITLE OF INVENTION: G PROTEIN-COUPLED RECEPTOR GENE CCR3 AND  
; TITLE OF INVENTION: ANTAGONISTS THEREOF  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/720,565  
; FILING DATE: 30-SEP-1996  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/00608  
; FILING DATE: 19-JAN-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/375,199  
; FILING DATE: 19-JAN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brook, David E.  
; REGISTRATION NUMBER: 22,592  
; REFERENCE/DOCKET NUMBER: LKS94-05A2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-861-6240  
; TELEFAX: 617-861-9540  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1193 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: Double  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA

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;
;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 92..1156
US-08-720-565-3

Query Match      68.6%; Score 35; DB 4; Length 1193;
Best Local Similarity 100.0%; Pred. No. 4,1e-10;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 TTGTGCTTATCCGGGCAAGAACTTATCGAATACA 51
Db 1 TTGTGCTTATCCGGGCAAGAACTTATCGAATACA 35

RESULT 2
US-09-422-978-9067
; Sequence 9067, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 9067
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..21_bind
; OTHER INFORMATION: downstream amplification primer 99-2170 for SEQ 1202, in complete
US-09-422-978-9067

Query Match      31.4%; Score 16; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GGTCTTCTTGCTTA 25
Db 1 GGTCTTCTTGCTTA 16

RESULT 3
US-09-634-238-126
; Sequence 126, Application US/09634238
; Patent No. 654772
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Havukkala, Ilkka J.
; APPLICANT: Bloksberg, Leonard, N.
; APPLICANT: Lubbers, Mark W.
; APPLICANT: Dekker, James
; APPLICANT: Christenson, Anna C.
; APPLICANT: Holland, Ross
; APPLICANT: O'Toole, Paul W.
; APPLICANT: Reid, Julian R.
; APPLICANT: Coolbear, Timothy
; TITLE OF INVENTION: Polynucleotides, materials incorporating
; FILE REFERENCE: 11000.1043U1
; CURRENT APPLICATION NUMBER: US/09/634,238
; CURRENT FILING DATE: 2000-08-08
; NUMBER OF SEQ ID NOS: 422
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 126
; LENGTH: 698
; TYPE: DNA
; ORGANISM: Lactobacillus rhamnosus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(698)
; OTHER INFORMATION: n = A,T,C or G
US-09-634-238-126

Query Match      31.4%; Score 16; DB 4; Length 698;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 TGGTCTTCTTGCTT 24
Db 550 TGGTCTTCTTGCTT 565

RESULT 4
US-08-635-066-1
; Sequence 1, Application US/08635066
; Patent No. 5945580
; GENERAL INFORMATION:
; APPLICANT: Dunsmuir, Pamela
; APPLICANT: Harpster, Mark H.
; TITLE OF INVENTION: Capsicum Hemicellulase Polynucleotides
; TITLE OF INVENTION: and Polypeptides
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/635,066
; FILING DATE: 19-APR-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 012176-005500
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2254 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 609..2129
US-08-635-066-1

Query Match      29.4%; Score 15; DB 2; Length 2254;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 TCTTCTTGTGCTTAT 26
Db 643 TCTTCTTGTGCTTAT 657
```



```
RESULT 5
US-09-134-000C-3185/c
; Sequence 3185, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032798-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3185
; LENGTH: 2787
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-3185

Query Match      29.4%; Score 15; DB 4; Length 2787;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 GGTCTTCTTGTCCT 24
      |||||||
DB      2353 GGTCTTCTTGTCCT 2339

RESULT 6
US-09-134-513-1
; Sequence 1, Application US/09134513
; Patent No. 6210964
; GENERAL INFORMATION:
; APPLICANT: Brown, Edward M.
; APPLICANT: Diaz, Ruben
; APPLICANT: Bai, Mei
; APPLICANT: Quinn, Stephen J.
; TITLE OF INVENTION: The Avian Extracellular Calcium-Sensing
; TITLE OF INVENTION: Receptor
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Vinson & Elkins L.L.P.
; STREET: 1455 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.
; ZIP: 20004-1008
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,513
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanzo, Michael A.
; REGISTRATION NUMBER: 36,912
; REFERENCE/DOCKET NUMBER: BRI331/13003
; TELEPHONE: (202)639-6585
; TELEFAX: (202)639-6604
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3177 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
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; HYPOTHETICAL: NO
US-09-134-513-1

Query Match      29.4%; Score 15; DB 3; Length 3177;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CTGGTCTTCTTGTC 22
      |||||||
DB      2176 CTGGTCTTCTTGTC 2190

RESULT 7
US-08-446-855A-1
; Sequence 1, Application US/08446855A
; Patent No. 5849573
; GENERAL INFORMATION:
; APPLICANT: Stewart, Thomas S
; APPLICANT: Flores, Maria V
; APPLICANT: O'Sullivan, William J
; TITLE OF INVENTION: Nucleotide sequence encoding carbamoyl
; TITLE OF INVENTION: phosphate synthetase II
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon & Vanderhye PC
; STREET: 1100 No. 5849573th Glebe Road, 8th Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,855A
; FILING DATE: 06-Jul-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mitchard, Leonard C
; REGISTRATION NUMBER: 29,009
; REFERENCE/DOCKET NUMBER: 47-80
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8920 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic
US-08-446-855A-1

Query Match      29.4%; Score 15; DB 2; Length 8920;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      33 AAGAACTTATCGAAA 47
      |||||||
DB      3831 AAGAACTTATCGAAA 3845

RESULT 8
US-09-150-741-1
; Sequence 1, Application US/09150741
; Patent No. 6183996
; GENERAL INFORMATION:
; APPLICANT: Stewart et al.
; TITLE OF INVENTION: Nucleotide Sequence Encoding Carbamoyl Phosphate
; Patent No. 6183996
; TITLE OF INVENTION: Synthetase II
```

```

; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/150,741
; CURRENT FILING DATE: 1998-09-10
; EARLIER APPLICATION NUMBER: PL6380
; EARLIER FILING DATE: 1992-12-16
; EARLIER APPLICATION NUMBER: AU93/00617
; EARLIER FILING DATE: 1993-12-02
; EARLIER APPLICATION NUMBER: 08/446,855
; EARLIER FILING DATE: 1995-07-06
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 8920
; TYPE: DNA
; ORGANISM: Plasmodium falciparum
US-09-150-741-1

Query Match          29.4%; Score 15; DB 3; Length 8920;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 AAGAACTTATCGAAA 47
Db 3831 AAGAACTTATCGAAA 3845

RESULT 9
US-09-497-855A-32/c
; Sequence 32, Application US/09497855A
; Patent No. 6605432
; GENERAL INFORMATION:
; APPLICANT: Huang, Tim
; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION
; FILE REFERENCE: UMO1523
; CURRENT APPLICATION NUMBER: US/09/497,855A
; CURRENT FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/120,592
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: 60/118,760
; PRIOR FILING DATE: 1999-02-05
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
; LENGTH: 118067
; TYPE: DNA
; ORGANISM: Homo sapiens;
US-09-497-855A-32

Query Match          29.4%; Score 15; DB 4; Length 118067;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TACACTGGTCTTCT 17
Db 113196 TACACTGGTCTTCT 113182

RESULT 10
US-08-469-260A-18
; Sequence 18, Application US/08469260A
; Patent No. 6451578
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,260A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: POREBSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-469-260A-18

Query Match          27.5%; Score 14; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 1e-02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 TCCGGCGCAAGAACT 39
Db 213 TCCGGCGCAAGAACT 226

RESULT 11
US-08-469-260A-20
; Sequence 20, Application US/08469260A
; Patent No. 6451578
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICANT: US/08/469,260A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/424,550  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: POREBSKI, PRISCILLA E.  
REGISTRATION NUMBER: 33,207  
REFERENCE/DOCKET NUMBER: 5527.PC.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 708-937-6365  
TELEFAX: 708-938-2623  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 281 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-469-260A-20

Query Match 27.5%; Score 14; DB 4; Length 281;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 TCCGGGCAAGAACT 39  
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DB 213 TCCGGGCAAGAACT 226

## RESULT 12

US-08-488-446-18  
Sequence 18, Application US/08488446  
Patent No. 6558898  
GENERAL INFORMATION:  
APPLICANT: JOHN N. SIMONS  
APPLICANT: TAMI J. PILOT-MATIAS  
APPLICANT: GEORGE J. DAWSON  
APPLICANT: GEORGE G. SCHLAUDER  
APPLICANT: SURESH M. DESAI  
APPLICANT: THOMAS P. LEARY  
APPLICANT: ANTHONY SCOTT MUEHROFF  
APPLICANT: JAMES C. ERKER  
APPLICANT: SHERI L. BULJK  
APPLICANT: ISA K. MUSHAWAR  
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS  
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE  
NUMBER OF SEQUENCES: 716  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D  
STREET: 100 ABBOTT PARK ROAD  
CITY: ABBOTT PARK  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/488,446  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/424,550  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: POREBSKI, PRISCILLA E.  
REGISTRATION NUMBER: 33,207  
REFERENCE/DOCKET NUMBER: 5527.PC.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 708-937-6365  
TELEFAX: 708-938-2623  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 281 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)

NAME: POREBSKI, PRISCILLA E.  
REGISTRATION NUMBER: 33,207  
REFERENCE/DOCKET NUMBER: 5527.PC.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 708-937-6365  
TELEFAX: 708-938-2623  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 281 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-488-446-18  
Query Match 27.5%; Score 14; DB 4; Length 281;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 TCCGGGCAAGAACT 39  
|||||  
DB 213 TCCGGGCAAGAACT 226

## RESULT 13

US-08-488-446-20  
Sequence 20, Application US/08488446  
Patent No. 6558898  
GENERAL INFORMATION:  
APPLICANT: JOHN N. SIMONS  
APPLICANT: TAMI J. PILOT-MATIAS  
APPLICANT: GEORGE J. DAWSON  
APPLICANT: GEORGE G. SCHLAUDER  
APPLICANT: SURESH M. DESAI  
APPLICANT: THOMAS P. LEARY  
APPLICANT: ANTHONY SCOTT MUEHROFF  
APPLICANT: JAMES C. ERKER  
APPLICANT: SHERI L. BULJK  
APPLICANT: ISA K. MUSHAWAR  
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS  
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE  
NUMBER OF SEQUENCES: 716  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D  
STREET: 100 ABBOTT PARK ROAD  
CITY: ABBOTT PARK  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/488,446  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/424,550  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: POREBSKI, PRISCILLA E.  
REGISTRATION NUMBER: 33,207  
REFERENCE/DOCKET NUMBER: 5527.PC.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 708-937-6365  
TELEFAX: 708-938-2623  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 281 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single

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; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-467-344A-20
; Sequence 20, Application US/08467344A
; Patent No. 6586568
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; TAMI J. PILOT-MATIAS
; GEORGE J. DAWSON
; GEORGE G. SCHLAUDER
; SURESH M. DESAI
; THOMAS P. LEARY
; ANTHONY SCOTT MUERHOFF
; JAMES C. ERKER
; SHERI L. BUIJK
; ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 07-Jun-1995
; APPLICATION NUMBER: US/08/467,344A
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/424,550
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
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US-08-467-344A-20
Query Match 27.5%; Score 14; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 TCCGGGCAAGAACT 39
| | | | | | | | | |
Db 213 TCCGGGCAAGAACT 226

RESULT 14
US-08-467-344A-18
; Sequence 18, Application US/08467344A
; Patent No. 6586568
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; TAMI J. PILOT-MATIAS
; GEORGE J. DAWSON
; GEORGE G. SCHLAUDER
; SURESH M. DESAI
; THOMAS P. LEARY
; ANTHONY SCOTT MUERHOFF
; JAMES C. ERKER
; SHERI L. BUIJK
; ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 07-Jun-1995
; APPLICATION NUMBER: US/08/467,344A
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/424,550
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-08-467-344A-18
Query Match 27.5%; Score 14; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 TCCGGGCAAGAACT 39
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Db 213 TCCGGGCAAGAACT 226

Search completed: August 2, 2004, 20:30:02
Job time : 52.4397 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 2, 2004, 18:06:45 ; Search time 2107.71 Seconds  
(without alignments)  
722.573 Million cell updates/sec

Title: US-10-068-067-16

Perfect score: 51

Sequence: 1 ggtaccactgtcttctgtt.....caagaacttatcgaaataca 51

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

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9: gb\_est1:\*  
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12: gb\_est3:\*  
13: gb\_est4:\*  
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16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
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20: em\_gss\_vrt:\*  
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23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rnd:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	18	35.3	584	14	CB390728
3	17	33.3	196	10	Bf153648
4	17	33.3	406	28	B40772 HS-1052-B1-

5	33.3	510	14	CD923067
6	33.3	523	12	BM375216
7	33.3	537	10	AW221092
8	33.3	577	9	AI772554
9	33.3	577	12	BG133271
10	33.3	598	29	CNS07HWS
11	33.3	610	14	CD925736
12	33.3	613	28	BH299085
13	33.3	647	12	BM160641
14	33.3	648	10	AW945046
15	33.3	672	14	CD911444
16	33.3	690	29	CE306183
17	33.3	780	29	CS06531
18	33.3	787	14	CD911445
19	33.3	905	10	BF340232
20	33.3	1203	12	BI764950
21	33.3	1828	12	BG297964
22	33.3	1828	9	AV162852
23	31.4	212	13	BQ282503
24	31.4	221	10	BF557219
25	31.4	224	9	AA957733
26	31.4	288	9	AV340346
27	31.4	318	29	CG407599
28	31.4	322	10	AW826871
29	31.4	346	12	BG738607
30	31.4	364	10	BF389025
31	31.4	404	10	BE344124
32	31.4	404	28	AQ825343
33	31.4	406	9	AI112888
34	31.4	406	12	BI179888
35	31.4	406	14	CD489747
36	31.4	420	29	CE669510
37	31.4	422	13	BX307267
38	31.4	430	14	CD489612
39	31.4	433	14	CB495381
40	31.4	433	14	CB495414
41	31.4	433	14	CB495567
42	31.4	436	13	BQ282505
43	31.4	451	13	BY505647
44	31.4	456	10	BF388753
45	31.4	458	14	CD489171

#### ALIGNMENTS

RESULT 1  
B1906283  
LOCUS 603063222F1 NIH\_MGC\_118 Homo sapiens cDNA clone IMAGE:5212541 5',  
DEFINITION mRNA sequence.  
ACCESSION B1906283  
VERSION B1906283.1 GI:16168946  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 876)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@mail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
Plate: LLAM1533 row: k column: 06  
High quality sequence stop: 800.

FEATURES  
source

Location/Qualifiers  
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/clone="IMAGE:5212541"  
/tissue\_type="leukocyte"  
/lab\_host="DH10B"  
/clone\_lib="NIH\_MGC\_118"  
/note="Vector: pCMV-SPORT6; Site:1: NotI; Site:2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 70.6%; Score 36; DB 12; Length 876;  
Best Local Similarity 100.0%; Pred. No. 1.5e+08;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CTGTGCTTATCCGGCAAGCAACTTATCGAATACA 36  
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RESULT 2  
LOCUS

CB390728 584 bp mRNA linear EST 15-MAY-2003  
DEFINITION OSTF39F9\_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.

ACCESSION CB390728  
VERSION CB390728.1 GI:30732438

## KEYWORDS

EST.

## SOURCE

Caenorhabditis elegans  
Caenorhabditis elegans  
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
Rhabditoides; Rhabditidae; Peloderinae; Caenorhabditis.

## REFERENCE

## AUTHORS

Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacot, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P.P., Pracek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H., Doucette-Stamm, L., Hill, D.E. and Vidal, M.  
C. elegans ORFome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein expression

## TITLE

Nat. Genet. (2003) In press

## JOURNAL

## COMMENT

Contact: Vidal M  
Marc Vidal Laboratory  
Dana Farber Cancer Institute  
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA  
Tel: 617 632 5180  
Fax: 617 632 5739  
Email: Marc.Vidal@fci.harvard.edu

Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFome cloning project; Contact David Hill@fci.harvard.edu or marc.vidal@fci.harvard.edu

POLYA-No.

FEATURES  
source

Location/Qualifiers  
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/mol\_type="mRNA"  
/strain="N2"  
/db\_xref="taxon:6239"  
/sex="Hermaphrodite and male"  
/tissue\_type="whole animal"  
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/clone\_lib="AD-wrmcDNA"

/note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

## ORIGIN

Query Match 35.3%; Score 18; DB 14; Length 584;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 TGTGCTTATCCGGCAAG 35  
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Db 233 TGTGCTTATCCGGCAAG 250  
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## RESULT 3

## LOCUS

BF153648 196 bp mRNA linear EST 11-SEP-2002  
DEFINITION 032A04 Mature tuber lambda ZAP Solanum tuberosum cDNA 5', mRNA sequence.

## ACCESSION

BF153648

## VERSION

BF153648.1 GI:11035588

## KEYWORDS

EST.

## SOURCE

Solanum tuberosum (potato)

## ORGANISM

Solanum tuberosum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum.

1 (bases 1 to 196)

Crookshanks, M., Emmeren, J., Welinder, K.G. and Nielsen, K.L.

The potato tuber transcriptome: analysis of 6077 expressed sequence tags

FEBS Lett. 506 (2), 123-126 (2001)

## JOURNAL

## MEDLINE

21475600

## PUBMED

11591384

## COMMENT

Contact: Karen G. Welinder

Institut for bioteknologi

Aalborg Universitet

Sohnsgaardsholmsvej 49, 9000 Aalborg, Denmark

Tel: +45 96358467

Fax: +45 98141808

Email: kgw@bio.au.dk

High quality sequence stop: 196

POLYA-No.

Location/Qualifiers

1..196

/organism="Solanum tuberosum"

/mol\_type="mRNA"

/cultivar="Field grown Kurat"

/db\_xref="taxon:4113"

/tissue\_type="tuber"

/clone\_lib="Mature tuber lambda ZAP"

/note="Vector: Lambda ZAP"

## ORIGIN

Query Match 33.3%; Score 17; DB 10; Length 196;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 TTCTTGCTTATCCGG 30  
|||||  
Db 153 TTCTTGCTTATCCGG 137  
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## RESULT 4

## LOCUS

B40772

## DEFINITION

HS-1052-B1-A05-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 774 Col=9 Row=B, genomic survey sequence.

## ACCESSION

B40772

## VERSION

B40772.1 GI:2545024

406 bp DNA linear GSS 18-OCT-1997  
HS-1052-B1-A05-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 774 Col=9 Row=B, genomic survey sequence.

ORIGIN

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pollination)"  
/clone\_lib="G750"

Query Match 33.3%; Score 17; DB 14; Length 510;  
Best Local Similarity 100.0%; Pred.No.1.7e-02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      QY    12 TCTTCTGTGCTATCC 28  
           ||||||  
DB        73 TCTTCTGTGCTATCC 89  
           ||||||

RESULT 6  
BM375216/c

LOCUS BM375216          523 bp    mRNA    EST 23-JUL-2002

DEFINITION EBem06\_SQ002\_L05\_R embryo\_21 DPA, no treatment, cv Optic, EBem06  
Hordeum vulgare subsp. vulgare cDNA clone EBem06\_SQ002\_L05 5', mRNA  
sequence.

ACCESSION BM375216

VERSION BM375216.2 GI:21935188

SOURCE EST.

ORGANISM Hordeum vulgare subsp. vulgare  
Hordeum vulgare subsp. vulgare  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Hordeum.  
1 (bases 1 to 523)  
Hedley,P., Liu,H., Caldwell,D., McCallum,N., Mudie,S., Cardle,L.,  
Ramsay,L., Machray,G., Marshall,D.F.M. and Waugh,R.  
Development of Barley Transcriptome Resources  
Unpublished (2001)

REFERENCE On Jan 10, 2002 this sequence version replaced gi:18118606.  
Contact: Waugh R, Marshall DF  
Genome Dynamics/Computational Biology  
Scottish Crop Research Institute  
Invergowrie, Dundee, DD2 5DA, Scotland, UK  
Tel.: 00 44 1382 562731  
Fax: 00 44 1382 562426  
Email: estescri.sari.ac.uk

JOURNAL All sequence has a Phred quality score of 20 or over  
Seq primer: M13 reverse.

FEATURES                      Location/Qualifiers  
source 1..523  
organism="Hordeum vulgare subsp. vulgare"  
mol\_type="mRNA"  
cultivar="Optic"  
sub\_species="vulgare"  
db\_xref="taxon:112509"  
clone="EBem06\_SQ002\_L05"  
tissue\_type="embryo"  
dev\_stage="21 DPA"  
lab\_host="DH10B"  
clone\_lib="Embryos, 21 DPA, no treatment, cv Optic,  
EBem06"  
notes=Vector: pSPORT1; Site 1: Sal I; Site 2: Not I;  
Non-normalised library, directionally cloned into pSPORT1.  
Derived from embryos dissected from developing grains (21  
days post anthesis) in glasshouse grown barley plants.  
Developed as part of the barley transcriptome resources of  
BSRC/SERAD funded cereal IGF (Investigating Gene  
Function) project."

ORIGIN

Query Match 33.3%; Score 17; DB 12; Length 523;  
Best Local Similarity 100.0%; Pred.No.1.7e-02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      QY    12 TCTTCTGTGCTATCC 28  
           ||||||





on stem with Agrobacterium tumefaciens C58 (Dr. T.J. Burr, Cornell U.). Galls were allowed to develop for another 4 wks, when gall tissue was frozen in liquid nitrogen."

## ORIGIN

Query Match 33.3%; Score 17; DB 12; Length 577;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 TTCTTGCTGCTTATCCGG 30  
Db 150 TTCTTGCTGCTTATCCGG 134

RESULT 10  
CNS07HW5/c

LOCUS 598 bp DNA linear GSS 03-OCT-2001  
DEFINITION Anopheles gambiae GSS T7 end of clone 31B05 of library NotreDamel from strain PEST of Anopheles gambiae (African malaria mosquito), genomic survey sequence.

ACCESSION AL611591  
VERSION AL611591.1 GI:15963014

KEYWORDS GSS.  
SOURCE Anopheles gambiae (African malaria mosquito)  
ORGANISM Anopheles gambiae

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.

REFERENCE 1 (bases 1 to 598)

## AUTHORS

## JOURNAL

Submitted (01-OCT-2001) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

REFERENCE 2 (bases 1 to 598)

## AUTHORS

## JOURNAL

Submitted (01-OCT-2001) BMFT, Institut Pasteur, 25, rue du Dr. Roux, Paris 75015, France  
This clone is from an A. Gambiae BAC library provided by P.H. Collins and sequenced by Genoscope in collaboration with the Laboratory of Biochem. and Biol. Molec. of Insects, Institut Pasteur.

## FEATURES

source

1..598  
/organism="Anopheles gambiae"  
/mol\_type="genomic DNA"  
/strain="PEST"  
/db\_xref="taxon:7165"  
/clone="31B05"  
/clone\_lib="NotreDamel"  
/note="end : 77"

## ORIGIN

Query Match 33.3%; Score 17; DB 29; Length 598;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 CTCTTGCTGCTTATCCG 29  
Db 75 CTCTTGCTGCTTATCCG 59

RESULT 11  
CD925736

LOCUS 610 bp mRNA linear EST 15-JUL-2003  
DEFINITION G750.118H11F010711 G750 Triticum aestivum cDNA clone G750118H11, mRNA sequence.

ACCESSION CD925736

VERSION CD925736.1 GI:32773500

## KEYWORDS

## SOURCE

Triticum aestivum (bread wheat)

## ORGANISM

Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Triticum.

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

Genoplatte, a major partnership french program in plant genomics  
Unpublished (2003)  
Contact: Genoplatte

Genoplatte

93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french plant genomics programme 'Genoplatte' (<http://www.genoplatte.com>) and <http://genoplatte-info.infobiogen.fr>.

## FEATURES

source

1..610  
/organism="Triticum aestivum"  
/mol\_type="mRNA"  
/cultivar="recital"  
/db\_xref="taxon:4565"  
/clone="G750118H11"  
/tissue\_type="grain (750 degrees per day after pollination)"  
/clone\_lib="G750"

## ORIGIN

Query Match 33.3%; Score 17; DB 14; Length 610;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 TCTTCTTGCTTATCC 28

Db 320 TCTTCTTGCTTATCC 336

## RESULT 12

## LOCUS

## DEFINITION

BH299085 613 bp DNA linear GSS 30-NOV-2001  
CH230-146H22.TJ CHORI-230 Segment 1 Rattus norvegicus genomic clone CH230-146H22, genomic survey sequence.

ACCESSION BH299085

VERSION BH299085.1 GI:17211493

## KEYWORDS

## SOURCE

## ORGANISM

Rattus norvegicus (Norway rat)  
Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

1 (bases 1 to 613)  
Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de Jong,P. and Fraser,C.W.  
Rat BAC End Sequences from Library CHORI-230 ECORI segment Unpublished (1999)

Other GSSs: CH230-146H22.TV

Contact: Shaving Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230

(<http://www.chori.org/bacpac/rat230.htm>). For BAC library

availability, please contact Pieter de Jong ([pdj@jgnc.org](mailto:pdj@jgnc.org)).

Clones may be purchased from BACPAC Resources

(<http://www.chori.org/bacpac/orering.information.htm>). BAC end

plate: [http://www.tigr.org/tldb/bac\\_ends/rat/bac\\_end\\_intro.html](http://www.tigr.org/tldb/bac_ends/rat/bac_end_intro.html)

Seq primer: SP6

Class: BAC ends.

Location/Qualifiers

```

source
1. .613
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="BN/SnHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-146H22"
/sex="Female"
/cell_type="Brain"
/clone_lib="CHORI-230 Segment 1"
/note="vector: pTARAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CHORI-230 Rat (BN/SnHsd/MCW) BAC library produced by
Pieter de Jong"

ORIGIN
Query Match          33.3%; Score 17; DB 28; Length 613;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCAGTGTCTTCTGTG 21
    |||||
Db 172 CCAGTGTCTTCTGTG 156

RESULT 13
BM160641
LOCUS
DEFINITION
EST563164 PYBS Plasmodium yoelii yoelii cDNA clone PYCJT89 5' end,
mRNA sequence.
ACCESSION
BM160641
VERSION
BM160641.1 GI:17306322
KEYWORDS
EST.
SOURCE
Plasmodium yoelii yoelii
ORGANISM
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE
1 (bases 1 to 647)
AUTHORS
Carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Vaidya,A.B.,
Fraser,C.M. and Carucci,D.J
TITLE
Plasmodium yoelii EST project at TIGR
JOURNAL
Unpublished (2001)
COMMENT
Contact: Jane Carlton
Parasite Genomics Group
The Institute for Genomic Research
712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-530-9319
Fax: 301-838-0208
Email: carlton@tigr.org
For clone info, please contact the Malaria Research and Reference
Reagent Resource Center, ATCC
http://www.malaria.mr4.org/mr4pages/index.html
Seq primer: ADF.

FEATURES
Location/Qualifiers
source
1..647
/organism="Plasmodium yoelii yoelii"
/mol_type="mRNA"
/strain="17XL"
/sub_species="yoelii"
/db_xref="taxon:73239"
/clone="PYCJT89"
/dev_stage="Asexual blood stages"
/lab_host="E. coli XL-1 Blue"
/clone_lib="PyBS"
/note="vector: PAD-GAL4; At 20-25% parasitemia, blood was
collected from BALB/cBYJ mice infected with Py17XL
parasites, and leukocytes removed by passage over
microcrystalline cellulose columns. Total RNA was
isolated using the guanidinium isothiocyanate method, and
mRNA isolated using oligo(dT)-cellulose chromatography.
First strand cDNA synthesis was completed using a 50-base
primer and reverse transcriptase in the presence of
5-methyl dCTP. After second strand synthesis, uneven
termini were treated with Pfu DNA polymerase and EcoRI
adaptors ligated to the blunt ends. The sample was cleaved
with XhoI and separated on a Sephacryl S-500 column.

```

```

ORIGIN
Query Match          33.3%; Score 17; DB 12; Length 647;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 35 GAACCTTATCGAATACA 51
    |||||
Db 139 GAACCTTATCGAATACA 155

RESULT 14
AW945046/c
LOCUS
DEFINITION
EST337096 tomato flower buds 3-8 mm, Cornell University
Lycopersicon esculentum cDNA clone cTOB12P18 5', mRNA sequence.
ACCESSION
AW945046
VERSION
AW945046.1 GI:8122797
KEYWORDS
EST.
SOURCE
Lycopersicon esculentum (tomato)
ORGANISM
Lycopersicon esculentum
REFERENCE
1 (bases 1 to 648)
AUTHORS
van der Hoeven,R.S., Bezzzredes,J.L., Matern,A.L., Holt,I.E.,
Liang,F., Hansen,I., Craven,M.B., Bowman,C.L., Romning,C.M.,
Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and
Tanksley,S.D.
TITLE
Generation of ESTs from tomato flower tissue, 3-8 mm buds
JOURNAL
Unpublished (1999)
COMMENT
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 Prime sequence.

FEATURES
Location/Qualifiers
source
1..648
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cTOB12P18"
/tissue_type="flower"
/dev_stage="3-8mm buds"
/clone_lib="tomato flower buds 3-8 mm, Cornell University"
/note="vector: pBlueScript SK(-); Site_1: EcoRI; Site_2:
XhoI; supplier: Tanksley; Flower buds and flowers were
taken from greenhouse plants (4-8 wks old, TA496). They
were immediately frozen in liquid nitrogen and then
size-separated while remaining frozen."

ORIGIN
Query Match          33.3%; Score 17; DB 10; Length 648;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 TTCTTGCTTATCCGG 30
    |||||
Db 141 TTCTTGCTTATCCGG 125

RESULT 15
CD911444
LOCUS
DEFINITION
G550.111C10F010521 G550 Triticum aestivum cDNA clone G55011C10,
mRNA sequence.

```

Size-fractionated cDNA was precipitated and ligated to HybriZAP arms directionally using EcoRI-XhoI cleaved arms. After packaging, the phagemid vector (PAD-GAL4) was excised from the HybriZAP vector and plasmid DNA isolated."

ACCESSION CD911444  
VERSION CD911444.1 GI:32685768  
KEYWORDS EST.  
SOURCE Triticum aestivum (bread wheat)  
ORGANISM Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Triticum.  
1 (bases 1 to 672)  
REFERENCE Genoplatne.  
AUTHORS Genoplatne, a major partnership french program in plant genomics  
TITLE Genoplatne, (2003)  
JOURNAL Unpublished (2003)  
COMMENT Contact: Genoplatne  
Genoplatne  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplatne' (<http://www.genoplatne.com>  
and <http://genoplatne-info.infobiogen.fr>).  
FEATURES  
source  
1..672  
    location/Qualifiers  
        /organism="Triticum aestivum"  
        /mol\_type="mRNA"  
        /cultivar="recital"  
        /db\_xref="taxon:4565"  
        /clone="G55011C10"  
        /tissue\_type="grain (550 degrees per day after  
            pollination)"  
        /clone\_lib="G550"  
ORIGIN  
Query Match 33.3%; Score 17; DB 14; Length 672;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 12 TCTTCTTGCTTATCC 28  
    |||||  
Db 250 TCTTCTTGCTTATCC 266  
Search completed: August 2, 2004, 20:27:58  
Job time : 2112.71 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 2, 2004, 16:56:38 ; Search time 246.207 seconds  
(without alignments)  
879.984 Million cell updates/sec

Title: US-10-068-067-16

Perfect score: 51

Sequence: 1 ggtaccactggtctcttctgt.....caagaacttatcgaataca 51

Scoring table: OLIGO.NUC

Gapop 60.0 , Gapext 60.0

Searched: 337863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N\_Geneseq\_29Jan04.\*

- 1: Geneseqn1980s.\*
- 2: Geneseqn1990s.\*
- 3: Geneseqn2000s.\*
- 4: Geneseqn2001as.\*
- 5: Geneseqn2001bs.\*
- 6: Geneseqn2002s.\*
- 7: Geneseqn2003as.\*
- 8: Geneseqn2003bs.\*
- 9: Geneseqn2003cs.\*
- 10: Geneseqn2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	51	100.0	51	6	ABQ78514	Nucleotid
2	51	100.0	51	6	ABQ78519	Nucleotid
3	51	100.0	2895	6	ABQ78513	Nucleotid
4	35	68.6	1193	2	AAT31335	CC-chemck
5	35	68.6	1193	2	AAV07403	Human C-C
6	22	43.1	22	6	ABQ78515	Nucleotid
7	22	43.1	22	6	ABQ78516	Nucleotid
8	22	43.1	22	6	ABQ78521	Nucleotid
9	21	41.2	21	6	ABQ78587	Nucleotid
10	21	41.2	21	6	ABQ78520	Nucleotid
11	21	41.2	21	6	ABQ78517	Nucleotid
12	17	33.3	3140	4	ABL12512	Drosophil
13	17	33.3	4400	4	ABL12414	Drosophil
14	16	31.4	21	3	AAZ74711	Human bia
15	16	31.4	265	7	ABX50975	Bovine ES
16	16	31.4	406	9	ADB51450	Primary r
17	16	31.4	586	4	ABA61111	Human foe
18	16	31.4	586	4	AAI41009	Probe #96
19	16	31.4	586	4	AAK35295	Human bon
20	16	31.4	586	4	AAK09404	Human bra
21	16	31.4	586	4	ABS35038	Human liv
22	16	31.4	601	3	AAF11306	Aspergill
23	16	31.4	661	3	AAF11272	Aspergill

C	24	16	31.4	823	5	ABV10808	Human pro
C	25	16	31.4	3153	7	ACA54065	Prokaryot
C	26	16	31.4	4563	7	AAD47607	Drosophil
C	27	16	31.4	5532	3	AAA81538	N. mening
C	28	16	31.4	7967	4	ABL18498	Drosophil
C	29	16	31.4	110000	3	AA81489_1	Continuation (2 of
C	30	16	31.4	349980	3	AAF21611_1	Neisseria
C	31	15	29.4	215	4	AAK79563	Human imm
C	32	15	29.4	240	3	AAAG1159	SEN virus
C	33	15	29.4	249	6	ABN16387	Human ORF
C	34	15	29.4	278	3	AAA61168	SEN virus
C	35	15	29.4	388	4	AAI92145	Human pol
C	36	15	29.4	489	2	AAI13914	Enterococ
C	37	15	29.4	489	6	ABS99709	Enterococ
C	38	15	29.4	537	3	AAK94557	Cat flea
C	39	15	29.4	646	3	AAK53290	Arabidops
C	40	15	29.4	700	4	AAH92754	Human inf
C	41	15	29.4	700	4	AAH92753	Human inf
C	42	15	29.4	864	7	ACF70596	Phototrab
C	43	15	29.4	1056	4	ABL25529	Drosophil
C	44	15	29.4	1076	3	AAK45720	Arabidops
C	45	15	29.4	1078	3	AAK41924	Arabidops

#### ALIGNMENTS

RESULT 1  
ABQ78514  
ID ABQ78514 standard; DNA; 51 BP.  
XX AC ABQ78514;  
XX DT 25-NOV-2002 (first entry)  
XX DB Nucleotide sequence of a regulatory sequence for human CCR3.  
XX KW Human; CC chemokine receptor 3; CCR3; allergic disorder; probe;  
XX KW inflammatory disorder; eosinophil; hypersensitivity; leukemia;  
XX KW infectious disorder; HIV; respiratory syncytial virus infection; ss.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
FT misc\_binding 24..27  
FT FT /\*tag= a  
FT FT /note= "transcription factor binding site for GATA"  
FT FT misc\_binding 40..43  
FT FT /\*tag= b  
FT FT /note= "transcription factor binding site for GATA"  
XX WO200262848-A2.  
XX 15-AUG-2002.  
XX 06-FEB-2002; 2002WO-US003442.  
XX 07-FEB-2002; 2001US-0267073P.  
XX 05-FEB-2002; 2002US-00068067.  
XX (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
XX Rothenberg ME, Zimmerman N;  
XX WPI; 2002-657524/70.  
XX New CC chemokine receptor 3 (CCR3) regulatory site in an untranslated  
XX exon 1, exon 2, exon 3 or promoter of a human CCR3 gene or mRNA capable  
XX of binding to regulatory elements, useful for preventing e.g. allergic  
XX inflammatory reactions.  
XX Claim 2; Page 25; 56pp; English.  
XX

CC The present sequence represents a probe for the human CC chemokine  
 CC receptor 3 (CCR3) gene. The probe comprises +10 to +60 of exon 1 of CCR3,  
 CC and is a regulatory sequence for CCR3. CCR3 is expressed on cells  
 CC involved in allergic and/or inflammatory disorders. The gene comprises 4  
 CC exons, with the coding region present on exon 4. The specification  
 CC describes methods of regulating the expression of CCR3. The regulatory  
 CC site is derived from an untranslated exon 1, exon 2, exon 3 or promoter  
 CC of a human CCR3 gene. Regulating the expression of the chemokine receptor  
 CC CCR3 is useful for preventing or treating disorders involving  
 CC eosinophils, such as allergic inflammatory and hypersensitivity  
 CC reactions, certain types of leukemia, and certain infectious disorders  
 CC involving CCR3, e.g. HIV or respiratory syncytial virus infection.  
 CC Expression and modulation of CCR3 is a useful tool in assessing  
 CC eosinophil targeting and in regulating eosinophil-mediated reactions and  
 CC diseases  
 XX SQ Sequence 51 BP; 13 A; 12 C; 11 G; 15 T; 0 U; 0 Other;

Query Match 100.0%; Score 51; DB 6; Length 51;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-18;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTACCACTGGTCTTCTGTGCTTATCCGGGCAAGAACTTATCGAATAACA 51  
 |||||  
 Db 1 GGTACCACTGGTCTTCTGTGCTTATCCGGGCAAGAACTTATCGAATAACA 51

## RESULT 2

ABQ78519  
 ID ABQ78519 standard; RNA; 51 BP.

XX AC ABQ78519;

XX DT 25-NOV-2002 (first entry)

XX DE Nucleotide sequence of a regulatory sequence for human CCR3.

XX KW Human; CC chemokine receptor 3; CCR3; allergic disorder; probe;  
 KW inflammatory disorder; eosinophil; hypersensitivity; leukemia;  
 KW infectious disorder; HIV; respiratory syncytial virus infection; ss.

XX OS Homo sapiens.

XX FN WO200262848-A2.

XX PD 15-AUG-2002.

XX PF 06-FEB-2002; 2002WO-US003442.

XX PR 07-FEB-2001; 2001US-0267073P.

XX PR 05-FEB-2002; 2002US-00068067.

XX PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.

XX PI Rothenberg ME, Zimmerman N;

XX DR WPI; 2002-657524/70.

XX PT New CC chemokine receptor 3 (CCR3) regulatory site in an untranslated  
 PT exon 1, exon 2, exon 3 or promoter of a human CCR3 gene or mRNA capable  
 PT of binding to regulatory elements, useful for preventing e.g. allergic  
 PT inflammatory reactions.

XX PS Claim 7; Page 56; 56pp; English.

XX CC The present sequence represents a probe for the human CC chemokine  
 CC receptor 3 (CCR3) gene. The probe is a regulatory sequence for CCR3. CCR3  
 CC is expressed on cells involved in allergic and/or inflammatory disorders.  
 CC The gene comprises 4 exons, with the coding region present on exon 4. The  
 CC specification describes methods of regulating the expression of CCR3. The  
 CC regulatory site is derived from an untranslated exon 1, exon 2, exon 3 or  
 CC promoter of a human CCR3 gene. Regulating the expression of the chemokine  
 CC receptor CCR3 is useful for preventing or treating disorders involving

CC eosinophils, such as allergic inflammatory and hypersensitivity  
 CC reactions, certain types of leukemia, and certain infectious disorders  
 CC involving CCR3, e.g. HIV or respiratory syncytial virus infection.  
 CC Expression and modulation of CCR3 is a useful tool in assessing  
 CC eosinophil targeting and in regulating eosinophil-mediated reactions and  
 CC diseases

XX SQ Sequence 51 BP; 13 A; 12 C; 11 G; 0 T; 15 U; 0 Other;

Query Match 100.0%; Score 51; DB 6; Length 51;

Best Local Similarity 70.6%; Pred. No. 1.2e-18;

Matches 36; Conservative 15; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTACCACTGGTCTTCTGTGCTTATCCGGGCAAGAACTTATCGAATAACA 51  
 |||||  
 Db 1 GGUACCAUGGUCUUCUGUGCUUACCGGCAAGAAUUGCUAAUACA 51

## RESULT 3

ABQ78513  
 ID ABQ78513 standard; DNA; 2895 BP.

XX AC ABQ78513;

XX DT 25-NOV-2002 (first entry)

XX DE Nucleotide sequence of the human CCR3 gene promoter.

XX KW Human; CC chemokine receptor 3; CCR3; allergic disorder;  
 KW inflammatory disorder; eosinophil; hypersensitivity; leukemia;  
 KW infectious disorder; HIV; respiratory syncytial virus infection;  
 KW promoter; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT misc\_signal 1640..1645

FT FT /tag= a

XX FT /note= "splice donor consensus site"

XX PN WO200262848-A2.

XX PD 15-AUG-2002.

XX PF 06-FEB-2002; 2002WO-US003442.

XX PR 07-FEB-2001; 2001US-0267073P.

XX PR 05-FEB-2002; 2002US-00068067.

XX PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.

XX PI Rothenberg ME, Zimmerman N;

XX DR WPI; 2002-657524/70.

XX PT New CC chemokine receptor 3 (CCR3) regulatory site in an untranslated  
 PT exon 1, exon 2, exon 3 or promoter of a human CCR3 gene or mRNA capable  
 PT of binding to regulatory elements, useful for preventing e.g. allergic  
 PT inflammatory reactions.

XX PS Disclosure; Fig 4; 56pp; English.

XX CC The present sequence represents the promoter of the human CC chemokine  
 CC receptor 3 (CCR3) gene. CCR3 is expressed on cells involved in allergic  
 CC and/or inflammatory disorders. The gene comprises 4 exons, with the  
 CC coding region present on exon 4. The specification describes methods of  
 CC regulating the expression of CCR3. The regulatory site is derived from an  
 CC untranslated exon 1, exon 2, exon 3 or promoter of a human CCR3 gene.  
 CC Regulating the expression of the chemokine receptor CCR3 is useful for  
 CC preventing or treating disorders involving eosinophils, such as allergic  
 CC inflammatory and hypersensitivity reactions, certain types of leukemia,  
 CC and certain infectious disorders involving CCR3, e.g. HIV or respiratory  
 CC syncytial virus infection. Expression and modulation of CCR3 is a useful

CC tool in assessing eosinophil targeting and in regulating eosinophil-mediated reactions and diseases

SQ Sequence 2895 BP; 829 A; 556 G; 920 T; 0 U; 0 Other;

Query Match 100.0%; Score 51; DB 6; Length 2895;  
Best Local Similarity 100.0%; Pred. No. 1.3e-18;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACCACTGGTCTTCTTGCTTATCCGGCAGAACTTATCGAAATACA 51  
|||||  
DB 1561 GGTACCACTGGTCTTCTTGCTTATCCGGCAGAACTTATCGAAATACA 1611

## RESULT 4

AAT31335

ID AAT31335 standard; cDNA; 1193 BP.

XX AAT31335;

XX 15-NOV-1996 (first entry)

XX CC-chemokine receptor 3 cDNA clone.

XX CC-chemokine receptor 3; CX3-3; Eos-L2; inhibitor; antisense;  
KW antiinflammatory; eosinophil; ss.

XX Homo sapiens.

XX Key Location/Qualifiers  
FH CDS 92..1159

FT /\*tag= a

FT variation

FT /\*tag= b

FT /note= "CCR-3 cDNA clone has GC at positions 918-919,  
coding for serine (AGC) at position 276; a genomic clone  
has CG at these positions, coding for threonine (AGC)"

XX WO9622371-A2.

XX 25-JUL-1996.

XX 19-JAN-1996; 96WO-US000608.

XX 19-JAN-1995; 95US-00375199.

XX (LEUK-) LEUKOSITE INC.

XX (BGHM ) BRIGHAM &amp; WOMENS HOSPITAL.

XX (CHIL-) CHILDRENS MEDICAL CENT.

PI Gerard CJ, Gerard NP, Mackay CR, Ponath PD, Post TW, Qin S;

XX WPI; 1996-354528/35.

DR P-PSDB; AAW03377.

XX Mammalian chemokine receptor-3 and related nucleic acids - useful to  
PT identify receptor inhibitors to treat inflammatory disease, e.g.  
PT autoimmune disorders, certain cancers, etc.

XX Claim 1; Page 111-113; 153pp; English.

XX A genomic DNA clone (AAT31335) codes for a novel receptor (AAW03377),  
CC designated Eos L2 or C-C chemokine receptor 3 (CCR-3), involved in  
CC leukocyte migration associated with inflammation. It was isolated from a  
CC human library constructed from eosinophils obtd. from a patient with  
CC hyper-eosinophilic syndrome using a probe (p4 cDNA) encoding the WIP-  
CC laipha/RANTES receptor. A CCR-3 genomic clone (AAT31334) was also  
CC isolated, and a consensus sequence is given in AAT31336. The cDNA and  
CC genomic clones can be used for the prodn. of recombinant CCR-3 in host  
CC cells, or to design antisense sequences useful for treating inflammatory  
CC disease

XX Sequence 1193 BP; 274 A; 310 C; 275 G; 334 T; 0 U; 0 Other;

Query Match 68.6%; Score 35; DB 2; Length 1193;  
Best Local Similarity 100.0%; Pred. No. 1.1e-09;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TTGTGCTTATCCGGCAGAACTTATCGAAATACA 51  
|||||  
DB 1 TTGTGCTTATCCGGCAGAACTTATCGAAATACA 35

## RESULT 5

AAV07403

ID AAV07403 standard; cDNA; 1193 BP.

XX AAV07403;

XX 28-SEP-1998 (first entry)

XX Human C-C chemokine receptor 3 cDNA.

XX C-C chemokine receptor 3; CCR3; CCR3; Eos L2; human;  
KW G protein-coupled receptor; leukocyte; antibody; antagonist;  
KW inflammation; allergy; asthma; graft rejection; infection;  
KW autoimmune disease; drug screening; therapy; ds.

XX Homo sapiens.

XX Key Location/Qualifiers  
FH CDS 92..1159

FT /\*tag= a

XX WO9814480-A1.

XX 09-APR-1998.

XX 24-SEP-1997; 97WO-US017103.

XX 30-SEP-1996; 96US-00720565.

XX (LEUK-) LEUKOSITE INC.

XX Mackay CR, Ponath PD;

XX WPI; 1998-286418/25.

DR P-PSDB; AAW51745.

XX Antibodies to chemokine receptor-3 protein - useful for diagnosis and  
PT treatment of inflammatory conditions, e.g. allergy, asthma, autoimmune  
PT disease, graft rejection or cancer.

XX Example 8; Page 134-136; 185pp; English.

XX This cDNA codes for novel human C-C chemokine receptor 3 (see AAW51745),  
CC also designated CCR-3, CCR3 or Eos L2, that binds and mediates chemotaxis  
CC in response to chemokines such as eotaxin, RANTES and MCP-3. The cDNA was  
CC isolated from a human eosinophil cDNA library constructed from  
CC eosinophils obtained from a patient with hyperesinophilic syndrome, and  
CC using CCR-1 cDNA as probe. A genomic DNA sequence (see AAV07402) is also  
CC provided as well as a consensus sequence (see AAV07404) for CCR-3. The  
CC invention relates to isolated and/or recombinant nucleic acids encoding  
CC CCR-3, isolated or recombinant CCR-3 polypeptides, recombinant nucleic  
CC acid constructs, host cells useful for production of recombinant CCR-3  
CC proteins, to antibodies reactive with the receptors, and to methods of  
CC using these products to identify ligands, antagonists and agonists of  
CC receptor function. Inhibitors of CCR-3 can be used to treat: inflammatory  
CC or allergic diseases and conditions, including respiratory allergic  
CC diseases such as asthma, allergic rhinitis, hypersensitivity lung  
CC disease, hypersensitivity pneumonitis, eosinophilic pneumonia (e.g.  
CC Loeffler's syndrome, chronic eosinophilic pneumonia, interstitial lung  
CC disease (ILD) e.g. idiopathic pulmonary fibrosis or ILD associated with  
CC rheumatoid arthritis, systemic lupus erythematosus, ankylosing  
CC spondylitis, systemic sclerosis, Sjogren's syndrome, polymyositis or  
CC dermatomyositis), systemic anaphylaxis or hypersensitivity responses,

CC drug allergy, insect sting allergy, inflammatory bowel disease, such as  
 CC Crohn's disease and ulcerative colitis, spondylarthropathy, scleroderma,  
 CC psoriasis, inflammatory dermatosis such as dermatitis, eczema, atopic  
 CC dermatitis, allergic contact dermatitis, urticaria, vasculitis (e.g.  
 CC necrotizing, cutaneous and hypersensitivity vasculitis); eosinophilic  
 CC myositis and eosinophilic fasciitis; autoimmune diseases such as  
 CC rheumatoid arthritis, psoriatic arthritis, multiple sclerosis, systemic  
 CC lupus erythematosus, myasthenia gravis, juvenile onset diabetes,  
 CC glomerulonephritis, autoimmune thyroiditis and Behcet's disease; graft  
 CC rejection, including allograft rejection or graft-versus-host disease;  
 CC cancers with leukocyte infiltration of the skin or organs; and also  
 CC reperfusion injury, atherosclerosis, certain haematologic malignancies,  
 CC septic shock and endotoxic shock. Promoters of CCR-3 function can be used  
 CC for treating: immunosuppression e.g. in AIDS patients or individuals  
 CC undergoing radiation therapy, chemotherapy, therapy for autoimmune  
 CC disease or other drug therapy, and immunosuppression due congenital  
 CC deficiency in receptor function or other causes; and infectious diseases  
 CC such as parasitic diseases, including helminth infections, such as  
 CC nematodes (round worms). The agents can also be used for detection and  
 CC diagnosis

XX Sequence 1193 BP; 274 A; 310 C; 275 G; 334 T; 0 U; 0 Other;  
 SQ

Query Match 58.6%; Score 35; DB 2; Length 1193;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-09;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TTGTGCTTATCCGGGCAAGAACTTATCGAATACA 51  
 DB 1 TTGTGCTTATCCGGGCAAGAACTTATCGAATACA 35

RESULT 6  
 ABQ78515  
 ID ABQ78515 standard; DNA; 22 BP.  
 AC ABQ78515;  
 XX  
 XX 25-NOV-2002 (first entry)  
 DT  
 XX  
 XX Nucleotide sequence of a regulatory sequence for human CCR3.  
 DE  
 XX Human; CC chemokine receptor 3; CCR3; allergic disorder; probe;  
 KW inflammatory disorder; eosinophil; hypersensitivity; leukemia;  
 KW infectious disorder; HIV; respiratory syncytial virus infection; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200262848-A2.  
 PN  
 XX 15-AUG-2002.  
 PD  
 XX 06-FEB-2002; 2002WO-US003442.  
 PF  
 XX 07-FEB-2001; 2001US-0267073P.  
 PR  
 XX 05-FEB-2002; 2002US-00068067.  
 XX  
 XX (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
 PA  
 XX  
 XX Rothenberg ME, Zimmerman N;  
 PI  
 XX WPI; 2002-657524/70.  
 DR  
 XX New CC chemokine receptor 3 (CCR3) regulatory site in an untranslated  
 PT exon 1, exon 2, exon 3 or promoter of a human CCR3 gene or mRNA capable  
 PT of binding to regulatory elements, useful for preventing e.g. allergic  
 PT inflammatory reactions.  
 XX  
 XX Claim 6; Page 54; 56pp; English.  
 PS  
 XX The present sequence represents a probe for the human CC chemokine  
 CC receptor 3 (CCR3) gene. The probe is a regulatory sequence for CCR3. CCR3  
 CC is expressed on cells involved in allergic and/or inflammatory disorders.

CC The gene comprises 4 exons, with the coding region present on exon 4. The  
 CC specification describes methods of regulating the expression of CCR3. The  
 CC regulatory site is derived from an untranslated exon 1, exon 2, exon 3 or  
 CC promoter of a human CCR3 gene. Regulating the expression of the chemokine  
 CC receptor CCR3 is useful for preventing or treating disorders involving  
 CC eosinophils, such as allergic inflammatory and hypersensitivity  
 CC reactions, certain types of leukemia, and certain infectious disorders  
 CC involving CCR3, e.g. HIV or respiratory syncytial virus infection.  
 CC Expression and modulation of CCR3 is a useful tool in assessing  
 CC eosinophil targeting and in regulating eosinophil-mediated reactions and  
 CC diseases

XX Sequence 22 BP; 2 A; 6 C; 6 G; 8 T; 0 U; 0 Other;

Query Match 43.1%; Score 22; DB 6; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 0.018;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACCACTGCTCTTCTTGTC 22  
 DB 1 GGTACCACTGCTCTTCTTGTC 22

RESULT 7  
 ABQ78516  
 ID ABQ78516 standard; DNA; 22 BP.  
 XX  
 AC ABQ78516;  
 XX  
 XX 25-NOV-2002 (first entry)  
 DT  
 XX  
 XX Nucleotide sequence of a regulatory sequence for human CCR3.  
 DE  
 XX Human; CC chemokine receptor 3; CCR3; allergic disorder; probe;  
 KW inflammatory disorder; eosinophil; hypersensitivity; leukemia;  
 KW infectious disorder; HIV; respiratory syncytial virus infection; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200262848-A2.  
 PN  
 XX 15-AUG-2002.  
 PD  
 XX 06-FEB-2002; 2002WO-US003442.  
 PF  
 XX 07-FEB-2001; 2001US-0267073P.  
 PR  
 XX 05-FEB-2002; 2002US-00068067.  
 XX  
 XX (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
 PA  
 XX  
 XX Rothenberg ME, Zimmerman N;  
 PI  
 XX WPI; 2002-657524/70.  
 DR  
 XX New CC chemokine receptor 3 (CCR3) regulatory site in an untranslated  
 PT exon 1, exon 2, exon 3 or promoter of a human CCR3 gene or mRNA capable  
 PT of binding to regulatory elements, useful for preventing e.g. allergic  
 PT inflammatory reactions.  
 XX  
 XX Claim 6; Page 54; 56pp; English.

CC The present sequence represents a probe for the human CC chemokine  
 CC receptor 3 (CCR3) gene. The probe is a regulatory sequence for CCR3. CCR3  
 CC is expressed on cells involved in allergic and/or inflammatory disorders.  
 CC The gene comprises 4 exons, with the coding region present on exon 4. The  
 CC specification describes methods of regulating the expression of CCR3. The  
 CC regulatory site is derived from an untranslated exon 1, exon 2, exon 3 or  
 CC promoter of a human CCR3 gene. Regulating the expression of the chemokine  
 CC receptor CCR3 is useful for preventing or treating disorders involving  
 CC eosinophils, such as allergic inflammatory and hypersensitivity  
 CC reactions, certain types of leukemia, and certain infectious disorders  
 CC involving CCR3, e.g. HIV or respiratory syncytial virus infection.  
 CC Expression and modulation of CCR3 is a useful tool in assessing



CC eosinophil targeting and in regulating eosinophil-mediated reactions and  
 CC diseases  
 XX Sequence 22 BP; 5 A; 5 C; 6 G; 6 T; 0 U; 0 Other;  
 SQ Query Match 43.1%; Score 22; DB 6; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 0.018;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CTTGTGCTTATCCGGCAAGAA 37  
 |||||  
 DB 1 CTTGTGCTTATCCGGCAAGAA 22

RESULT 8  
 ABQ78521  
 ID ABQ78521 standard; RNA; 22 BP.  
 XX  
 AC ABQ78521;  
 XX  
 DT 25-NOV-2002 (first entry)  
 XX  
 DE Nucleotide sequence of a regulatory sequence for human CCR3.  
 XX  
 KW Human; CC chemokine receptor 3; CCR3; allergic disorder; probe;  
 KW inflammatory disorder; eosinophil; hypersensitivity; leukemia;  
 KW infectious disorder; HIV; respiratory syncytial virus infection; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200262848-A2.  
 XX  
 PD 15-AUG-2002.  
 XX  
 PF 06-FEB-2002; 2002WO-US003442.  
 XX  
 PR 07-FEB-2001; 2001US-0267073P.  
 PR 05-FEB-2002; 2002US-00068067.  
 XX  
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
 XX  
 PI Rothenberg ME, Zimmerman N;  
 XX  
 DR WPI; 2002-657524/70.  
 XX  
 XX New CC chemokine receptor 3 (CCR3) regulatory site in an untranslated  
 PT exon 1, exon 2, exon 3 or promoter of a human CCR3 gene or mRNA capable  
 PT of binding to regulatory elements, useful for preventing e.g. allergic  
 PT inflammatory reactions.  
 XX  
 PS Claim 8; Page 56; 56pp; English.  
 XX  
 CC The present sequence represents a probe for the human CC chemokine  
 CC receptor 3 (CCR3) gene. The probe is a regulatory sequence for CCR3. CCR3  
 CC is expressed on cells involved in allergic and/or inflammatory disorders.  
 CC The gene comprises 4 exons, with the coding region present on exon 4. The  
 CC specification describes methods of regulating the expression of CCR3. The  
 CC regulatory site is derived from an untranslated exon 1, exon 2, exon 3 or  
 CC promoter of a human CCR3 gene. Regulating the expression of the chemokine  
 CC receptor CCR3 is useful for preventing or treating disorders involving  
 CC eosinophils, such as allergic inflammation and hypersensitivity  
 CC reactions, certain types of leukemia, and certain infectious disorders  
 CC involving CCR3, e.g. HIV or respiratory syncytial virus infection.  
 CC Expression and modulation of CCR3 is a useful tool in assessing  
 CC eosinophil targeting and in regulating eosinophil-mediated reactions and  
 CC diseases  
 XX Sequence 22 BP; 5 A; 5 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 43.1%; Score 22; DB 6; Length 22;  
 Best Local Similarity 72.7%; Pred. No. 0.018;  
 Matches 16; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 16 CTTGTGCTTATCCGGCAAGAA 37  
 |||||  
 DB 1 CUUGUCUUUAUCCGGCAAGAA 22

RESULT 9  
 ABQ78587  
 ID ABQ78587 standard; RNA; 21 BP.  
 XX  
 AC ABQ78587;  
 XX  
 DT 25-NOV-2002 (first entry)  
 XX  
 DE Nucleotide sequence of a regulatory sequence for human CCR3.  
 XX  
 KW Human; CC chemokine receptor 3; CCR3; allergic disorder; probe;  
 KW inflammatory disorder; eosinophil; hypersensitivity; leukemia;  
 KW infectious disorder; HIV; respiratory syncytial virus infection; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200262848-A2.  
 XX  
 PD 15-AUG-2002.  
 XX  
 PF 06-FEB-2002; 2002WO-US003442.  
 XX  
 PR 07-FEB-2001; 2001US-0267073P.  
 PR 05-FEB-2002; 2002US-00068067.  
 XX  
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
 XX  
 PI Rothenberg ME, Zimmerman N;  
 XX  
 DR WPI; 2002-657524/70.  
 XX  
 XX New CC chemokine receptor 3 (CCR3) regulatory site in an untranslated  
 PT exon 1, exon 2, exon 3 or promoter of a human CCR3 gene or mRNA capable  
 PT of binding to regulatory elements, useful for preventing e.g. allergic  
 PT inflammatory reactions.  
 XX  
 PS Claim 8; Page 56; 56pp; English.  
 XX  
 CC The present sequence represents a probe for the human CC chemokine  
 CC receptor 3 (CCR3) gene. The probe is a regulatory sequence for CCR3. CCR3  
 CC is expressed on cells involved in allergic and/or inflammatory disorders.  
 CC The gene comprises 4 exons, with the coding region present on exon 4. The  
 CC specification describes methods of regulating the expression of CCR3. The  
 CC regulatory site is derived from an untranslated exon 1, exon 2, exon 3 or  
 CC promoter of a human CCR3 gene. Regulating the expression of the chemokine  
 CC receptor CCR3 is useful for preventing or treating disorders involving  
 CC eosinophils, such as allergic inflammation and hypersensitivity  
 CC reactions, certain types of leukemia, and certain infectious disorders  
 CC involving CCR3, e.g. HIV or respiratory syncytial virus infection.  
 CC Expression and modulation of CCR3 is a useful tool in assessing  
 CC eosinophil targeting and in regulating eosinophil-mediated reactions and  
 CC diseases  
 XX Sequence 21 BP; 10 A; 4 C; 3 G; 0 T; 4 U; 0 Other;

Query Match 41.2%; Score 21; DB 6; Length 21;  
 Best Local Similarity 81.0%; Pred. No. 0.066;  
 Matches 17; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 31 GCAAGAACTTATCGAATAACA 51  
 |||||  
 DB 1 GCAAGAACTTATCGAATAACA 21

RESULT 10  
 ABQ78520  
 ID ABQ78520 standard; RNA; 21 BP.  
 XX

```

AC ABQ78520;
XX
DT 25-NOV-2002 (first entry)
XX
DE Nucleotide sequence of a regulatory sequence for human CCR3.
XX
KW Human; CC chemokine receptor 3; CCR3; allergic disorder; probe;
KW inflammatory disorder; eosinophil; hypersensitivity; leukemia;
KW infectious disorder; HIV; respiratory syncytial virus infection; ss.
XX
OS Homo sapiens.
XX
FN WO200262848-A2.
XX
PD 15-AUG-2002.
XX
PF 06-FEB-2002; 2002WO-US003442.
XX
PR 07-FEB-2001; 2001US-0267073P.
XX
PR 05-FEB-2002; 2002US-00068067.
XX
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
XX
PI Rothenberg ME, Zimmerman N;
XX
DR WPI; 2002-657524/70.
XX
XX
PT New CC chemokine receptor 3 (CCR3) regulatory site in an untranslated
PT exon 1, exon 2, exon 3 or promoter of a human CCR3 gene or mRNA capable
PT of binding to regulatory elements, useful for preventing e.g. allergic
PT inflammatory reactions.
XX
PS Claim 8; Page 56; 56pp; English.
XX
CC The present sequence represents a probe for the human CC chemokine
CC receptor 3 (CCR3) gene. The probe is a regulatory sequence for CCR3. CCR3
CC is expressed on cells involved in allergic and/or inflammatory disorders.
CC The gene comprises 4 exons, with the coding region present on exon 4. The
CC specification describes methods of regulating the expression of CCR3. The
CC regulatory site is derived from an untranslated exon 1, exon 2, exon 3 or
CC promoter of a human CCR3 gene. Regulating the expression of the chemokine
CC receptor CCR3 is useful for preventing or treating disorders involving
CC eosinophils, such as allergic inflammatory and hypersensitivity
CC reactions, certain types of leukemia, and certain infectious disorders
CC involving CCR3, e.g. HIV or respiratory syncytial virus infection.
CC Expression and modulation of CCR3 is a useful tool in assessing
CC eosinophil targeting and in regulating eosinophil-mediated reactions and
CC diseases
XX
SQ Sequence 21 BP; 2 A; 5 C; 6 G; 0 T; 8 U; 0 Other;
Query Match 41.2%; Score 21; DB 6; Length 21;
Best Local Similarity 61.9%; Pred. No. 0.066;
Matches 13; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTAACACTGGTCTCTGTG 21
Db 1 GGUACACUGGUCUCUGUG 21

RESULT 11
ABQ78517
ID ABQ78517 standard; DNA; 21 BP.
XX
AC ABQ78517;
XX
DT 25-NOV-2002 (first entry)
XX
DE Nucleotide sequence of a regulatory sequence for human CCR3.
XX
KW Human; CC chemokine receptor 3; CCR3; allergic disorder; probe;
KW inflammatory disorder; eosinophil; hypersensitivity; leukemia;
KW infectious disorder; HIV; respiratory syncytial virus infection; ss.
XX
OS Homo sapiens.
XX
FN WO200262848-A2.
XX
PD 15-AUG-2002.
XX
PF 06-FEB-2002; 2002WO-US003442.
XX
PR 07-FEB-2001; 2001US-0267073P.
XX
PR 05-FEB-2002; 2002US-00068067.
XX
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
XX
PI Rothenberg ME, Zimmerman N;
XX
DR WPI; 2002-657524/70.
XX
XX
PT New CC chemokine receptor 3 (CCR3) regulatory site in an untranslated
PT exon 1, exon 2, exon 3 or promoter of a human CCR3 gene or mRNA capable
PT of binding to regulatory elements, useful for preventing e.g. allergic
PT inflammatory reactions.
XX
PS Claim 8; Page 56; 56pp; English.
XX
CC The present sequence represents a probe for the human CC chemokine
CC receptor 3 (CCR3) gene. The probe is a regulatory sequence for CCR3. CCR3
CC is expressed on cells involved in allergic and/or inflammatory disorders.
CC The gene comprises 4 exons, with the coding region present on exon 4. The
CC specification describes methods of regulating the expression of CCR3. The
CC regulatory site is derived from an untranslated exon 1, exon 2, exon 3 or
CC promoter of a human CCR3 gene. Regulating the expression of the chemokine
CC receptor CCR3 is useful for preventing or treating disorders involving
CC eosinophils, such as allergic inflammatory and hypersensitivity
CC reactions, certain types of leukemia, and certain infectious disorders
CC involving CCR3, e.g. HIV or respiratory syncytial virus infection.
CC Expression and modulation of CCR3 is a useful tool in assessing
CC eosinophil targeting and in regulating eosinophil-mediated reactions and
CC diseases
XX
SQ Sequence 21 BP; 2 A; 5 C; 6 G; 0 T; 8 U; 0 Other;
Query Match 41.2%; Score 21; DB 6; Length 21;
Best Local Similarity 61.9%; Pred. No. 0.066;
Matches 13; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTAACACTGGTCTCTGTG 21
Db 1 GGUACACUGGUCUCUGUG 21

RESULT 12
ABQ78517/c
ID ABQ78517 standard; cDNA; 3140 BP.
XX
AC ABQ78517;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 32018.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
OS Drosophila melanogaster.
XX
FN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.

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PR 11-JUL-2000; 2000US-00614150.  
XX (PEKE ) PE CORP NY.  
XX  
XX Venter JC, Adams M, Li PWD, Myers EW;  
XX  
XX WPI; 2001-656860/75.  
DR P-PSDB; ABB68409.  
XX  
XX New isolated nucleic acid detection reagent for detecting 1000 or more  
PT genes from Drosophila and for elucidating cell signaling and cell-cell  
PT interactions.  
PT  
XX Claim 1; SEQ ID NO 32018; 21pp + Sequence Listing; English.  
XX  
XX The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from Drosophila. The invention is  
CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-  
CC ABB72072). The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 3140 BP; 789 A; 738 C; 769 G; 844 T; 0 U; 0 Other;  
SQ  
Query Match 33.3%; Score 17; DB 4; Length 3140;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 33 AAGAACTTATCGAAATA 49  
DB 2243 AAGAACTTATCGAAATA 2227  
  
RESULT 13  
ID ABL12414/c  
XX ABL12414 standard; cDNA; 4400 BP.  
XX  
XX ABL12414;  
XX  
XX 26-MAR-2002 (first entry)  
XX  
XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 31724.  
XX  
XX Drosophila; developmental biology; cell signalling; insecticide;  
KW pharmaceutical; gene; ss.  
XX  
XX Drosophila melanogaster.  
OS  
XX WO200171042-A2.  
XX  
XX 27-SEP-2001.  
XX  
XX 23-MAR-2001; 2001WO-US009231.  
XX  
XX 23-MAR-2000; 2000US-0191637P.  
PR  
XX 11-JUL-2000; 2000US-00614150.  
XX  
XX (PEKE ) PE CORP NY.  
XX  
XX Venter JC, Adams M, Li PWD, Myers EW;  
XX  
XX WPI; 2001-656860/75.  
DR P-PSDB; ABB68311.  
XX  
XX New isolated nucleic acid detection reagent for detecting 1000 or more  
PT genes from Drosophila and for elucidating cell signaling and cell-cell  
PT interactions.  
PT  
XX Claim 1; SEQ ID NO 31724; 21pp + Sequence Listing; English.  
PS

XX The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from Drosophila. The invention is  
CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-  
CC ABB72072). The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 4400 BP; 1037 A; 1066 C; 1109 G; 1188 T; 0 U; 0 Other;  
SQ  
Query Match 33.3%; Score 17; DB 4; Length 4400;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 33 AAGAACTTATCGAAATA 49  
DB 765 AAGAACTTATCGAAATA 749  
  
RESULT 14  
ID AAZ74711  
XX AAZ74711 standard; DNA; 21 BP.  
XX  
XX AAZ74711;  
XX  
XX 10-SEP-2001 (first entry)  
XX  
XX Human biallelic marker downstream amplification primer SEQ ID NO:9067.  
XX  
XX Human genome; biallelic marker; high density disequilibrium map;  
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;  
KW haplotyping; hybridisation; identification; characterisation;  
KW amplification; single nucleotide polymorphism; SNP; PCR primer;  
KW diagnosis; ss.  
XX  
XX Homo sapiens.  
OS  
XX WO9954500-A2.  
XX  
XX 28-OCT-1999.  
XX  
XX 21-APR-1999; 99WO-IB000822.  
XX  
XX 21-APR-1998; 98US-0082614P.  
PR  
XX 23-NOV-1998; 98US-0109732P.  
XX  
XX (GEST ) GENSET.  
XX  
XX Cohen D, Blumenfeld M, Chumakov I;  
XX  
XX WPI; 2000-013267/01.  
XX  
XX Novel biallelic markers used to construct a high density disequilibrium  
PT map of the human genome.  
PT  
XX Claim 8; Page 2164; 2745pp; English.  
XX  
XX AAZ65654 to AAZ69578 represent human biallelic markers from the present  
CC invention, which contain a polymorphic base at position 24 of their  
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification  
CC primers for the biallelic markers. The biallelic markers of the invention  
CC have a variety of uses: they can be used for high density mapping of the  
CC human genome, and in complex association studies and haplotyping studies  
CC which are useful in determining the genetic basis for disease states.  
CC Compositions and methods of the invention can also be useful for the  
CC identification of the targets for the development of pharmaceutical  
CC agents and diagnostic methods, as well as the characterisation of the  
CC differential efficacious responses to and side effects from  
CC pharmaceutical agents acting on a disease as well as other treatment.

CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and  
 CC 3367, are not actually given a sequence in the Sequence Listing from the  
 CC Present invention

XX SQ Sequence 21 BP; 4 A; 4 C; 5 G; 8 T; 0 U; 0 Other;  
 Query Match 31.4%; Score 16; DB 3; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 41;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 10 GGTCCTCTTGCTTA 25  
 Db 1 GGTCCTCTTGCTTA 16  
 |||||

RESULT 15  
 ABX50975/c  
 ID ABX50975 standard; cDNA; 265 BP.

XX AC ABX50975;

XX 25-FEB-2003 (first entry)

XX DE Bovine EST associated with lactation/muscle/fat deposition #904.

XX KW Bovine; ss; EST; expressed sequence tag; lactation; LMPD;  
 KW muscle deposition; fat deposition; genome mapping; gene identification;  
 XX gene analysis; cattle breeding.

XX OS Bos Taurus.

XX PN US2002137160-A1.

XX PD 26-SEP-2002.

XX PF 26-OCT-2001; 2001US-00983965.

XX PR 17-DEC-1998; 98US-0113678P.

XX PR 15-DEC-1999; 99US-00465231.

XX PA (BYAT/) BYATT J C.

XX PA (MATH/) MATHIALAGAN N.

XX PA (TAON/) TAO N.

XX PA (WARR/) WARREN W C.

XX PI Byatt JC, Mathialagan N, Tao N, Warren WC;

XX DR MPI; 2003-102386/09.

XX PT Purified nucleic acid molecules, useful for genome mapping, gene  
 PT identification and analysis, cattle breeding or preparation of constructs  
 PT for cattle gene expression and genetically improved cattle.

XX PS Claim 2; SEQ ID NO 904; 38pp; English.

XX The invention relates to a purified nucleic acid molecule associated with  
 CC lactation or muscle and fat deposition (designated LMPD) derived from  
 CC cattle, and the LMPD nucleic acid can specifically hybridise to a second  
 CC nucleic acid molecule comprising any of 5912 nucleotide sequences,  
 CC appearing as ABX50072-ABX55983, or complements of them. Also included are  
 CC ; (1) a transformed cell having a nucleic acid comprising an LMPD nucleic  
 CC acid linked to a promoter and a 3' non- translated sequence that  
 CC functions in the cell to cause termination of transcription and addition  
 CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and  
 CC (2) determining a level or pattern of a molecule in a bovine cell or  
 CC tissue comprising: (a) incubating a marker nucleic acid (comprising any  
 CC of the 5912 nucleic acid sequences or its complement or fragment) with a  
 CC complementary nucleic acid molecule obtained from the bovine cell or  
 CC tissue, where hybridisation between the marker nucleic acid and the  
 CC complementary nucleic acid permits the detection of the molecule; and (b)  
 CC detecting the level or pattern of the complementary nucleic acid, where  
 CC the detection of the complementary nucleic acid is predictive of the  
 CC level or pattern of the molecule. The LMPD nucleic acid is used for

CC determining a level or pattern of a molecule in a bovine cell or tissue.  
 CC It is useful for genome mapping, gene identification and analysis, cattle  
 CC breeding, preparation of constructs for use in cattle gene expression, or  
 CC for genetically improving cattle. The present sequence is one of the 5912  
 CC bovine LMPD EST (expressed sequence tag) nucleic acids. Note: The present  
 CC sequence was not shown in the specification but was obtained in  
 CC electronic format from the USPTO web site:  
 CC seqdata.uspto.gov/sequence.html?DocID=20020137160

XX SQ Sequence 265 BP; 67 A; 72 C; 67 G; 59 T; 0 U; 0 Other;

Query Match 31.4%; Score 16; DB 7; Length 265;

Best Local Similarity 100.0%; Pred. No. 42;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 16 CTTGTGCTTATCCGGG 31

Db 217 CTTGTGCTTATCCGGG 202  
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Search completed: August 2, 2004, 18:24:21  
 Job time : 249.207 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 2, 2004, 16:56:11 ; Search time 248 Seconds  
(without alignments)  
1008.307 Million cell up.

Title: US-10-068-067-16

Perfect score: 51  
Sequence: 1 ggtaccactgggtctctctgt.....caagaacttatcgaaataca 51

Scoring table: IDENTITY\_NUC  
Gapop 10.0 ; Gapext 1.0

Searched: 3222919 seqs. 2451570024 residues

Total number of hits satisfying chosen parameters: 6445838

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45

Database :

- 1: /cgn2\_6/pdata1/1/pubnba/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/pdata1/1/pubnba/PCT\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/pdata1/1/pubnba/US05\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/pdata1/1/pubnba/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/pdata1/1/pubnba/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/pdata1/1/pubnba/PCTUS\_PUBCOMB.seq.\*
- 7: /cgn2\_6/pdata1/1/pubnba/US08\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/pdata1/1/pubnba/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/pdata1/1/pubnba/US09A\_PUBCOMB.seq.\*
- 10: /cgn2\_6/pdata1/1/pubnba/US09B\_PUBCOMB.seq.\*
- 11: /cgn2\_6/pdata1/1/pubnba/US09C\_PUBCOMB.seq.\*
- 12: /cgn2\_6/pdata1/1/pubnba/US09\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/pdata1/1/pubnba/US09\_NEW\_PUB.seq.\*
- 14: /cgn2\_6/pdata1/1/pubnba/US10A\_PUBCOMB.seq.\*
- 15: /cgn2\_6/pdata1/1/pubnba/US10B\_PUBCOMB.seq.\*
- 16: /cgn2\_6/pdata1/1/pubnba/US10C\_PUBCOMB.seq.\*
- 17: /cgn2\_6/pdata1/1/pubnba/US10\_NEW\_PUB.seq.\*
- 18: /cgn2\_6/pdata1/1/pubnba/US50\_NEW\_PUB.seq.\*
- 19: /cgn2\_6/pdata1/1/pubnba/US50\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	51	100.0	51	14	US-10-068-067-16	Sequence 16, App
2	51	100.0	51	14	US-10-068-067-21	Sequence 21, App
3	51	100.0	2895	14	US-10-068-067-11	Sequence 11, App
4	35	68.6	1193	15	US-10-083-028-3	Sequence 3, Appli
5	26	51.0	394	13	US-10-085-783A-39054	Sequence 39054, A
6	26	51.0	394	16	US-10-042-535A-39054	Sequence 39054, A
7	25	49.0	396	13	US-10-085-783A-38805	Sequence 38805, A
8	25	49.0	396	16	US-10-042-535A-38805	Sequence 38805, A
9	24.4	47.8	669	13	US-10-027-632-201530	Sequence 201530, A
10	24.4	47.8	669	16	US-10-027-632-201530	Sequence 201530, A
11	24.4	47.8	1312	13	US-10-027-632-201531	Sequence 201531, A
12	24.4	47.8	1312	16	US-10-027-632-201531	Sequence 201531, A
13	23.4	45.9	611	13	US-10-027-632-214974	Sequence 214974, A
14	23.4	45.9	611	16	US-10-027-632-214974	Sequence 214974, A

15	23.4	45.9	1327	17	US-10-437-963-20957	Sequence 20957, A
16	23.4	45.9	1349	13	US-10-027-632-251334	Sequence 251334, A
C 16	23.4	45.9	1349	16	US-10-027-632-251334	Sequence 251334, A
18	22.6	44.3	1135	13	US-10-424-599-18358	Sequence 18358, A
19	22.4	43.9	565	13	US-10-027-632-128025	Sequence 128025, A
20	22.4	43.9	565	16	US-10-027-632-128025	Sequence 128025, A
21	22.4	43.9	576	13	US-10-027-632-256503	Sequence 256503, A
22	22.4	43.9	576	13	US-10-027-632-256504	Sequence 256504, A
23	22.4	43.9	576	16	US-10-027-632-256503	Sequence 256503, A
24	22.4	43.9	576	16	US-10-027-632-256504	Sequence 256504, A
25	22.4	43.9	584	13	US-10-027-632-131371	Sequence 131371, A
26	22.4	43.9	584	16	US-10-027-632-131371	Sequence 131371, A
27	22.4	43.9	1343	15	US-10-078-770-107	Sequence 107, App
28	22.4	43.9	1343	15	US-10-078-770-107	Sequence 115, App
29	22.4	43.9	1372	13	US-10-428-114-17357	Sequence 17357, A
30	22.4	43.9	2170	13	US-10-428-114-24889	Sequence 24889, A
31	22.4	43.9	2277	13	US-10-425-114-15509	Sequence 15509, A
32	22.2	43.5	1719	9	US-09-974-300-648	Sequence 648, App
33	22.2	43.5	1861	9	US-09-822-830A-4	Sequence 4, Appli
34	22.2	43.5	2000	16	US-10-260-238-2606	Sequence 2606, App
35	22.2	43.5	2782	9	US-09-764-864-268	Sequence 268, App
36	22.2	43.5	2784	9	US-09-764-864-167	Sequence 167, App
37	22.2	43.5	3050	13	US-10-087-192-1025	Sequence 1025, App
38	22.2	43.5	60500	13	US-10-087-192-1024	Sequence 1024, App
39	22	43.1	22	14	US-10-068-067-17	Sequence 17, Appli
40	22	43.1	22	14	US-10-068-067-18	Sequence 18, Appli
41	22	43.1	22	14	US-10-068-067-23	Sequence 23, Appli
42	22	43.1	467	13	US-10-085-783A-38234	Sequence 38234, A
43	22	43.1	467	16	US-10-243-535A-38234	Sequence 38234, A
C 44	22	43.1	92880	17	US-09-997-722-217	Sequence 217, App
C 45	21.8	42.7	80462	17	US-10-332-281-7	Sequence 7, Appli

## ALIGNMENTS

```

RESULT 1
US-10-068-067-16
/ Sequence 16, Application US/10068067
/ Publication No. US20020151064A1
/ GENERAL INFORMATION:
/ APPLICANT: Rothenberg, Marc E.
/ APPLICANT: Zimmermann, Nives
/ APPLICANT: Children's Hospital Med
/ TITLE OF INVENTION: REGULATION OF C
/ FILE REFERENCE: CMC-153
/ CURRENT APPLICATION NUMBER: US/10/0
/ CURRENT FILING DATE: 2002-02-05
/ PRIOR APPLICATION NUMBER: 60/367,07
/ PRIOR FILING DATE: 2001-02-07
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 16
/ LENGTH: 51
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-068-067-16

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Query Match      100.0%; Score 51; DB 14; Length 51;
Best Local Similarity 100.0%; Pred. No. 9.4e-12;
Matches 51; Conservative 0; Mismatches 0; Indels 0;

QY 1 GGTACCACTGGCTCTCTTGTGTTATCGGGCAAGAACATTTCGAAATACA 51
Db 1 GGTACCACTGGCTCTCTTGTGTTATCGGGCAAGAACATTTCGAAATACA 51

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RESULT 2  
US-10-068-067-21  
; Sequence 21, Application US/10068067  
; Publication No. US20020151064A1  
; GENERAL INFORMATION:  
; APPLICANT: Rothenberg, Marc E.

APPLICANT: Zimmermann, Nives  
TITLE OF INVENTION: Children's Hospital Medical Center  
FILE REFERENCE: CMC-153  
CURRENT APPLICATION NUMBER: US/10/068,067  
CURRENT FILING DATE: 2002-02-05  
PRIOR APPLICATION NUMBER: 60/267,073  
PRIOR FILING DATE: 2001-02-07  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 21  
LENGTH: 51  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-10-068-067-21

Query Match 100.0%; Score 51; DB 14; Length 51;  
Best Local Similarity 70.6%; Pred. No. 9.4e-12;  
Matches 35; Conservative 15; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTACCACTGGTCTTCTGTGCTTATCCGGGCAAGAACTTATCGAAATACA 51  
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
Db 1 GGUACCACUGGUCUUCUGUGCUUAUCCGGGCAAGAACTTATCGAAATACA 51

RESULT 3  
US-10-068-067-11  
Sequence 11, Application US/10068067  
Publication No. US20020151064A1  
GENERAL INFORMATION:  
APPLICANT: Rothenberg, Marc E.  
APPLICANT: Zimmermann, Nives  
TITLE OF INVENTION: Regulation of CCR3 Expression  
FILE REFERENCE: CMC-153  
CURRENT APPLICATION NUMBER: US/10/068,067  
CURRENT FILING DATE: 2002-02-05  
PRIOR APPLICATION NUMBER: 60/267,073  
PRIOR FILING DATE: 2001-02-07  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 11  
LENGTH: 2895  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-068-067-11

Query Match 100.0%; Score 51; DB 14; Length 2895;  
Best Local Similarity 100.0%; Pred. No. 3.1e-11;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTACCACTGGTCTTCTGTGCTTATCCGGGCAAGAACTTATCGAAATACA 51  
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Db 1561 GGTACCACTGGTCTTCTGTGCTTATCCGGGCAAGAACTTATCGAAATACA 1611

RESULT 4  
US-10-283-028-3  
Sequence 3, Application US/10283028  
Publication No. US20030143684A1  
GENERAL INFORMATION:  
APPLICANT: Gerard, Craig J.  
Gerard, No. US20030143684A1ma P.  
Mackay, Charles R.  
Ponath, Paul D.  
Post, Theodore W.  
Qin, Shixin  
TITLE OF INVENTION: G PROTEIN-COUPLED RECEPTOR GENE CCR3 AND  
ANTAGONISTS THEREOF  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive

CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/283,028  
FILING DATE: 28-Oct-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/720,565  
FILING DATE: 30-SEP-1996  
APPLICATION NUMBER: PCT/US96/00608  
FILING DATE: 19-JAN-1996  
APPLICATION NUMBER: US 08/375,199  
FILING DATE: 19-JAN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Brook, David E.  
REGISTRATION NUMBER: 22,592  
REFERENCE/DOCKET NUMBER: LKS94-05A2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1193 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 92..1156  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-10-283-028-3

Query Match 68.6%; Score 35; DB 15; Length 1193;  
Best Local Similarity 100.0%; Pred. No. 0.00017;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 TTGTGCTTATCCGGGCAAGAACTTATCGAAATACA 51  
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Db 1 TTGTGCTTATCCGGGCAAGAACTTATCGAAATACA 35

RESULT 5  
US-10-085-783A-39054/c  
Sequence 39054, Application US/10085783A  
Publication No. US20040037841A1  
GENERAL INFORMATION:  
APPLICANT: ChondroGene Inc.  
APPLICANT: Liew, C.C.  
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
FILE REFERENCE: 4231/2002  
CURRENT APPLICATION NUMBER: US/10/085,783A  
CURRENT FILING DATE: 2002-02-28  
PRIOR APPLICATION NUMBER: US 60/305,340  
PRIOR FILING DATE: 2001-07-13  
PRIOR APPLICATION NUMBER: US 60/275,017  
PRIOR FILING DATE: 2001-03-12  
PRIOR APPLICATION NUMBER: US 60/271,955  
PRIOR FILING DATE: 2001-02-28  
NUMBER OF SEQ ID NOS: 58994  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 39054  
LENGTH: 394  
TYPE: DNA  
ORGANISM: Human  
FEATURE:

NAME/KEY: misc\_feature  
LOCATION: (67)..(67)  
OTHER INFORMATION: n is a, c, g, or t  
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NAME/KEY: misc\_feature  
LOCATION: (109)..(109)  
OTHER INFORMATION: n is a, c, g, or t  
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NAME/KEY: misc\_feature  
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NAME/KEY: misc\_feature  
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NAME/KEY: misc\_feature  
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OTHER INFORMATION: n is a, c, g, or t  
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NAME/KEY: misc\_feature  
LOCATION: (393)..(393)  
OTHER INFORMATION: n is a, c, g, or t

US-10-085-783A-39054  
Query Match 51.0%; Score 26; DB 13; Length 394;  
Best Local Similarity 72.7%; Pred. No. 0.86;  
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 3 TACCAGTCTCTTCTGTGCTTATCCGGCAAGAACTTATCGAA 46  
DB 366 TANCACAGATTACTTGTTCTTACCCCAAGTAAGATTATAGAA 323  
RESULT 6  
US-10-242-535A-39054/c  
; Sequence 39054, Application US/10242535A  
; Publication No. US20040013663A1  
; GENERAL INFORMATION:  
; APPLICANT: ChondroGene Inc.  
; APPLICANT: Liew, C.C.  
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
; FILE REFERENCE: 4231/2005  
; CURRENT APPLICATION NUMBER: US 10/242,535A  
; CURRENT FILING DATE: 2002-09-12  
; PRIOR APPLICATION NUMBER: US 10/085,783  
; PRIOR FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: US 60/305,340  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US 60/275,017  
; PRIOR FILING DATE: 2001-03-12  
; PRIOR APPLICATION NUMBER: US 60/271,955  
; PRIOR FILING DATE: 2001-02-28  
; NUMBER OF SEQ ID NOS: 58994  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 39054  
; LENGTH: 394.  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (67)..(67)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (109)..(109)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (145)..(145)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (168)..(168)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (187)..(187)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (193)..(193)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (204)..(204)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (224)..(224)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (269)..(269)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (277)..(277)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (287)..(287)

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; OTHER INFORMATION: n is a, c, g, or t
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; NAME/KEY: misc feature
; LOCATION: (306)..(306)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (314)..(314)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (348)..(348)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (364)..(364)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (370)..(370)
; OTHER INFORMATION: n is a, c, g, or t
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; NAME/KEY: misc feature
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; OTHER INFORMATION: n is a, c, g, or t
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US-10-242-535A-39054

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Query Match 51.0%; Score 26; DB 16; Length 394;
Best Local Similarity 72.7%; Pred.No. 0.86;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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Qy 3 TACCACGTGCTCTTCTGCTTATCCGGCGCAAGACTTATCGAA 46
Db 366 TACACAGATTACTTGTCTTCTGCTTATCCGGCGCAAGACTTATCGAA 323

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## RESULT 7

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US-10-085-783A-38805/c
; Sequence 38805, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.

```

```

; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis

```

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; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38805
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (67)..(67)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (109)..(109)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (145)..(145)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature

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; LOCATION: (168)..(168)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (187)..(187)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (193)..(193)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (204)..(204)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (224)..(224)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (269)..(269)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (277)..(277)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (287)..(287)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (314)..(314)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (348)..(348)
; OTHER INFORMATION: n is a, c, g, or t
;
US-10-085-783A-38805

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Query Match 49.0%; Score 25; DB 13; Length 396;
Best Local Similarity 70.5%; Pred.No. 2.3;
Matches 31; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

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Qy 3 TACCACGTGCTCTTCTGCTTATCCGGCGCAAGACTTATCGAA 46
Db 366 TACACAGATTACTTGTCTTCTGCTTATCCGGCGCAAGACTTATCGAA 323

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## RESULT 8

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US-10-242-535A-38805/c
; Sequence 38805, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.

```

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; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38805
; LENGTH: 396
; TYPE: DNA

```



ORGANISM: Human  
FEATURE: NAME/KEY: misc\_feature  
LOCATION: (67)..(67)  
OTHER INFORMATION: n is a, c, g, or t  
FEATURE: NAME/KEY: misc\_feature  
LOCATION: (109)..(109)  
OTHER INFORMATION: n is a, c, g, or t  
FEATURE: NAME/KEY: misc\_feature  
LOCATION: (145)..(145)  
OTHER INFORMATION: n is a, c, g, or t  
FEATURE: NAME/KEY: misc\_feature  
LOCATION: (168)..(168)  
OTHER INFORMATION: n is a, c, g, or t  
FEATURE: NAME/KEY: misc\_feature  
LOCATION: (187)..(187)  
OTHER INFORMATION: n is a, c, g, or t  
FEATURE: NAME/KEY: misc\_feature  
LOCATION: (193)..(193)  
OTHER INFORMATION: n is a, c, g, or t  
FEATURE: NAME/KEY: misc\_feature  
LOCATION: (204)..(204)  
OTHER INFORMATION: n is a, c, g, or t  
FEATURE: NAME/KEY: misc\_feature  
LOCATION: (224)..(224)  
OTHER INFORMATION: n is a, c, g, or t  
FEATURE: NAME/KEY: misc\_feature  
LOCATION: (269)..(269)  
OTHER INFORMATION: n is a, c, g, or t  
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LOCATION: (277)..(277)  
OTHER INFORMATION: n is a, c, g, or t  
FEATURE: NAME/KEY: misc\_feature  
LOCATION: (287)..(287)  
OTHER INFORMATION: n is a, c, g, or t  
FEATURE: NAME/KEY: misc\_feature  
LOCATION: (314)..(314)  
OTHER INFORMATION: n is a, c, g, or t  
FEATURE: NAME/KEY: misc\_feature  
LOCATION: (348)..(348)  
OTHER INFORMATION: n is a, c, g, or t  
US-10-242-535A-38805

Query Match 49.0%; Score 25; DB 16; Length 396;  
Best Local Similarity 70.5%; Pred. No. 2.3;  
Matches 31; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

Qy 3 TACCACTGCTCTTCTTGCTTATCCGGGCAAGAACTTATCGAA 46  
Db 366 TACACACATTACTTGTCTTCTAGTCAAGTAAATTATAGAA 323

RESULT 9  
US-10-027-632-201530/c  
; Sequence 201530, Application US/10027632  
; Publication No. US20020198371A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; TITLE OF INVENTION: Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.129

; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 201530  
; LENGTH: 669  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-201530

Query Match 47.8%; Score 24.4; DB 13; Length 669;  
Best Local Similarity 73.8%; Pred. No. 4.9;  
Matches 31; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 1 GGTACCACTGCTCTTCTTGCTTATCCGGGCAAGAACTTAT 42  
Db 284 GATAAGCCTGCTCTTTTGTGCTTCTCGGGCAATAATGTGT 243

RESULT 10  
US-10-027-632-201530/c  
; Sequence 201530, Application US/10027632  
; Publication No. US20030204075A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; TITLE OF INVENTION: Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 201530  
; LENGTH: 669  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-201530

Query Match 47.8%; Score 24.4; DB 16; Length 669;  
Best Local Similarity 73.8%; Pred. No. 4.9;  
Matches 31; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 1 GGTACCACTGCTCTTCTTGCTTATCCGGGCAAGAACTTAT 42  
Db 284 GATAAGCCTGCTCTTTTGTGCTTCTCGGGCAATAATGTGT 243

RESULT 11  
 US-10-027-632-201531/c  
 ; Sequence 201531, Application US/10027632  
 ; Publication No. US20020198371A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, David G.  
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
 ; TITLE OF INVENTION: Polymorphisms in the Human Genome  
 ; FILE REFERENCE: 108827.129  
 ; CURRENT APPLICATION NUMBER: US/10/027,632  
 ; CURRENT FILING DATE: 2002-04-30  
 ; PRIOR APPLICATION NUMBER: US 60/218,006  
 ; PRIOR FILING DATE: 2000-07-12  
 ; PRIOR APPLICATION NUMBER: US 60/198,676  
 ; PRIOR FILING DATE: 2000-04-20  
 ; PRIOR APPLICATION NUMBER: US 60/193,483  
 ; PRIOR FILING DATE: 2000-03-29  
 ; PRIOR APPLICATION NUMBER: US 60/185,218  
 ; PRIOR FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: US 60/167,363  
 ; PRIOR FILING DATE: 1999-11-23  
 ; PRIOR APPLICATION NUMBER: US 60/156,358  
 ; PRIOR FILING DATE: 1999-09-28  
 ; PRIOR APPLICATION NUMBER: US 60/146,002  
 ; PRIOR FILING DATE: 1999-08-09  
 ; NUMBER OF SEQ ID NOS: 325720  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 201531  
 ; LENGTH: 1312  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 ; FEATURE:  
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 ; LOCATION: (1)...(1312)  
 ; OTHER INFORMATION: n = A,T,C or G  
 US-10-027-632-201531

Query Match 47.8%; Score 24.4; DB 13; Length 1312;  
 Best Local Similarity 73.8%; Pred. No. 5.9;  
 Matches 31; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 GGTAACCACTGCTCTTCTGTGCTTATCCGGGCAAGAACTTAT 42  
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 Db 284 GATAAGCCTGCTCTTCTGTGCTTATCCGGGCAAGAACTTATGT 243

RESULT 12  
 US-10-027-632-201531/c  
 ; Sequence 201531, Application US/10027632  
 ; Publication No. US200204075A9  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, David G.  
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
 ; TITLE OF INVENTION: Polymorphisms in the Human Genome  
 ; FILE REFERENCE: 108827.129  
 ; CURRENT APPLICATION NUMBER: US/10/027,632  
 ; CURRENT FILING DATE: 2002-04-30  
 ; PRIOR APPLICATION NUMBER: US 60/218,006  
 ; PRIOR FILING DATE: 2000-07-12  
 ; PRIOR APPLICATION NUMBER: US 60/198,676  
 ; PRIOR FILING DATE: 2000-04-20  
 ; PRIOR APPLICATION NUMBER: US 60/193,483  
 ; PRIOR FILING DATE: 2000-03-29  
 ; PRIOR APPLICATION NUMBER: US 60/185,218  
 ; PRIOR FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: US 60/167,363  
 ; PRIOR FILING DATE: 1999-11-23  
 ; PRIOR APPLICATION NUMBER: US 60/156,358  
 ; PRIOR FILING DATE: 1999-09-28  
 ; PRIOR APPLICATION NUMBER: US 60/146,002  
 ; PRIOR FILING DATE: 1999-08-09

; NUMBER OF SEQ ID NOS: 325720  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 201531  
 ; LENGTH: 1312  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 ; FEATURE:  
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 ; LOCATION: (1)...(1312)  
 ; OTHER INFORMATION: n = A,T,C or G  
 US-10-027-632-201531

Query Match 47.8%; Score 24.4; DB 16; Length 1312;  
 Best Local Similarity 73.8%; Pred. No. 5.9;  
 Matches 31; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 GGTAACCACTGCTCTTCTGTGCTTATCCGGGCAAGAACTTAT 42  
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 Db 284 GATAAGCCTGCTCTTCTGTGCTTATCCGGGCAAGAACTTATGT 243

RESULT 13  
 US-10-027-632-214974  
 ; Sequence 214974, Application US/10027632  
 ; Publication No. US20020198371A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, David G.  
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
 ; TITLE OF INVENTION: Polymorphisms in the Human Genome  
 ; FILE REFERENCE: 108827.129  
 ; CURRENT APPLICATION NUMBER: US/10/027,632  
 ; CURRENT FILING DATE: 2002-04-30  
 ; PRIOR APPLICATION NUMBER: US 60/218,006  
 ; PRIOR FILING DATE: 2000-07-12  
 ; PRIOR APPLICATION NUMBER: US 60/198,676  
 ; PRIOR FILING DATE: 2000-04-20  
 ; PRIOR APPLICATION NUMBER: US 60/193,483  
 ; PRIOR FILING DATE: 2000-03-29  
 ; PRIOR APPLICATION NUMBER: US 60/185,218  
 ; PRIOR FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: US 60/167,363  
 ; PRIOR FILING DATE: 1999-11-23  
 ; PRIOR APPLICATION NUMBER: US 60/156,358  
 ; PRIOR FILING DATE: 1999-09-28  
 ; PRIOR APPLICATION NUMBER: US 60/146,002  
 ; PRIOR FILING DATE: 1999-08-09  
 ; NUMBER OF SEQ ID NOS: 325720  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 214974  
 ; LENGTH: 611  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (1)...(611)  
 ; OTHER INFORMATION: n = A,T,C or G  
 US-10-027-632-214974

Query Match 45.9%; Score 23.4; DB 13; Length 611;  
 Best Local Similarity 67.3%; Pred. No. 13;  
 Matches 33; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 3 TACCACCTGCTCTTCTGTGCTTATCCGGGCAAGAACTTATCGAATACA 51  
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 Db 199 TATCAATGGGCTTTTCTGTGCTTATCGAATACA 247

RESULT 14  
 US-10-027-632-214974  
 ; Sequence 214974, Application US/10027632  
 ; Publication No. US200204075A9  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, David G.

Db 512 TACCACTCCGCTTATATGCTTCCAGGGTGACTGCTTCTCCTAATACA 560

Search completed: August 2, 2004, 18:14:49  
Job time : 250 secs

3 TACCACCTGGCTCTCTTGTGCTTATCCGGGCAAGAACTTATCGAAATACA 51  
199 TATCAATGGGCTTTTCTTGTGGCCTGACACCTGACTTATGGAAATAAA 247

Query Match	45.9%	Score 23.4;	DB 17;	Length 1327;
Best Local Similarity	67.3%;	Pred. No. 16;		
Matches 33:	Conservative	0;	Mismatches 16:	Indels 0;
				Gaps 0;

3 TACCACTGGTCTCTTGTGCTTATCCGGGCAAGAACTTATCGAAATACA 51

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 2, 2004, 16:05:29 ; Search time 47 Seconds  
(without alignments)  
602.181 Million cell updates/sec

Title: US-10-068-067-15

Perfect score: 51  
Sequence: 1 ggtaccactggtcttctgt.....caagaacttcgaataaca 51

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 27747546 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq.\*  
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5: /cgn2\_6/ptodata/2/ina/PTCUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	68.6	1193	4	US-08-720-565-3
2	22	43.1	1341	4	US-09-543-681A-1577
3	21.4	42.0	912	4	US-09-420-786A-4
4	21	41.2	2521	4	US-09-620-312D-777
5	21	41.2	4021	4	US-09-453-702B-197
6	20.8	40.8	987	4	US-09-599-360B-58
7	20.8	40.8	13440	4	US-08-961-527-128
8	20.6	40.4	2553	4	US-09-328-352-2457
9	20.4	40.0	1000	4	US-09-280-116-134
10	20.2	39.6	1023	1	US-08-785-065-2
11	20.2	39.6	1023	4	US-09-151-412-2
12	20.2	39.6	4775	4	US-09-220-132-5
13	20	39.2	675	3	US-08-821-994-52
14	20	39.2	690	3	US-08-821-994-53
15	20	39.2	897	3	US-08-899-330-14
16	20	39.2	1026	4	US-09-655-908-19
17	20	39.2	1102	3	US-08-821-994-86
18	20	39.2	1434	3	US-08-821-994-62
19	19.8	38.8	1119	4	US-09-489-039A-6787
20	19.8	38.8	1131	4	US-09-107-532A-3259
21	19.8	38.8	1231	4	US-09-454-279-13
22	19.8	38.8	1827	4	US-09-543-681A-3546
23	19.8	38.8	1827	4	US-08-448-194-5
24	19.8	38.8	2809	3	US-08-867-921-5
25	19.8	38.8	3114	4	US-09-543-681A-3505
26	19.8	38.8	3286	2	US-08-363-124A-1
27	19.6	38.4	500	4	US-09-669-751-168

ALIGNMENTS

RESULT 1  
US-08-720-565-3  
; Sequence 3, Application US/08720565  
; Patent No. 6537764  
; GENERAL INFORMATION:  
; APPLICANT: Gerard, Craig J.  
; APPLICANT: Gerard, No. 6537764ma P.  
; APPLICANT: Mackay, Charles R.  
; APPLICANT: Ponath, Paul D.  
; APPLICANT: Post, Theodore W.  
; APPLICANT: Qin, Shixin  
; TITLE OF INVENTION: G PROTEIN-COUPLED RECEPTOR GENE CCR3 AND  
; TITLE OF INVENTION: ANTAGONISTS THEREOF  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/720,565  
; FILING DATE: 30-SEP-1996  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/00608  
; FILING DATE: 19-JAN-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/375,199  
; FILING DATE: 19-JAN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brook, David E.  
; REGISTRATION NUMBER: 22,592  
; REFERENCE/DOCKET NUMBER: LKS94-05A2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-861-9540  
; TELEFAX: 617-861-9540  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1193 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: Double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna

28	19.6	38.4	597	4	US-09-621-976-3245	Sequence 3245, Ap
29	19.6	38.4	982	4	US-09-221-017B-7	Sequence 7, Appli
30	19.6	38.4	28720	4	US-09-341-587-7	Sequence 7, Appli
31	19.6	38.4	84495	4	US-09-797-906-3	Sequence 3, Appli
32	19.6	38.4	1664976	4	US-08-916-421B-1	Sequence 1, Appli
33	19.4	38.0	268	4	US-09-313-294A-3259	Sequence 3259, Ap
34	19.4	38.0	549	1	US-08-367-198A-4	Sequence 4, Appli
35	19.4	38.0	655	4	US-09-023-655-98	Sequence 98, Appli
36	19.4	38.0	970	1	US-08-367-198A-1	Sequence 1, Appli
37	19.4	38.0	1257	4	US-09-328-352-1178	Sequence 1178, Ap
38	19.4	38.0	129908	4	US-09-585-858-1	Sequence 1, Appli
39	19.4	38.0	1230025	4	US-09-198-452A-1	Sequence 1, Appli
40	19.2	37.6	339	4	US-09-489-039A-5353	Sequence 5353, Ap
41	19.2	37.6	461	4	US-09-621-976-2698	Sequence 2698, Ap
42	19.2	37.6	483	4	US-09-328-352-131	Sequence 131, App
43	19.2	37.6	505	4	US-09-621-976-3341	Sequence 3341, App
44	19.2	37.6	580	4	US-09-221-017B-278	Sequence 278, App
45	19.2	37.6	1413	4	US-09-489-039A-5890	Sequence 5890, Ap

DB 388 ACCATGCTCTTCTGGTCTCTTTCTGGCTGAAATTTAT 426

FEATURE:  
NAME/KEY: CDS  
LOCATION: 92..1156  
US-08-720-565-3

Query Match 68.6%; Score 35; DB 4; Length 1193;  
Best Local Similarity 100.0%; Pred. No. 1.2e-05;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TTGTGCTTATCCGGCAAGAACTTATCGAAATACA 51  
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DB 1 TTGTGCTTATCCGGCAAGAACTTATCGAAATACA 35  
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RESULT 2  
US-09-543-681A-1577  
; Sequence 1577, Application US/09543681A  
; Patent No. 6605709  
; GENERAL INFORMATION:  
; APPLICANT: GARY BRETON  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
; FILE REFERENCE: 2709.1002-001  
; CURRENT APPLICATION NUMBER: US/09/543,681A  
; PRIOR FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/128,706  
; PRIOR FILING DATE: 1999-04-09  
; NUMBER OF SEQ ID NOS: 344  
; SEQ ID NO 1577  
; LENGTH: 1341  
; TYPE: DNA  
; ORGANISM: Proteus mirabilis  
US-09-543-681A-1577

Query Match 43.1%; Score 22; DB 4; Length 1341;  
Best Local Similarity 67.4%; Pred. No. 5.5;  
Matches 31; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 3 TACCACTGGTCTTCTGTGCTTATCCGGCAAGAACTTATCGAAAT 48  
|||||  
DB 1008 TAAATTTGATCTCTTGTAGGACTTACCCCAAGAACTTATCGAAAT 1053  
|||||

RESULT 3  
US-09-420-786A-4  
; Sequence 4, Application US/09420786A  
; Patent No. 6410717  
; GENERAL INFORMATION:  
; APPLICANT: FURUSAWA, Iwao  
; TITLE OF INVENTION: A GENE ENCODING A HOST FACTOR PROTEIN INDISPENSABLE FOR  
; TITLE OF INVENTION: MULTIPLICATION OF A PLANT VIRUS  
; FILE REFERENCE: 026350-030  
; CURRENT APPLICATION NUMBER: US/09/420,786A  
; CURRENT FILING DATE: 1999-10-19  
; PRIOR APPLICATION NUMBER: JP 10-301810  
; PRIOR FILING DATE: 1998-10-23  
; PRIOR APPLICATION NUMBER: JP 11-232678  
; PRIOR FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana heynh  
US-09-420-786A-4

Query Match 42.0%; Score 21.4; DB 4; Length 912;  
Best Local Similarity 71.8%; Pred. No. 8.8;  
Matches 28; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 4 ACCACTGGTCTTCTGTGCTTATCCGGCAAGAACTTAT 42  
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RESULT 4  
US-09-620-312D-777/c  
; Sequence 777, Application US/09620312D  
; Patent No. 6569662  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Zhang, Jie  
; APPLICANT: Ren, Feiyan  
; APPLICANT: Chen, Rui-hong  
; APPLICANT: Zhao, Qing A.  
; APPLICANT: Wehrman, Tom  
; APPLICANT: Xue, Aidong J.  
; APPLICANT: Yang, Yonghong  
; APPLICANT: Wang, Jian-Rui  
; APPLICANT: Zhou, Ping  
; APPLICANT: Ma, Yundong  
; APPLICANT: Wang, Dunrui  
; APPLICANT: Wang, Zhiwei  
; APPLICANT: John Tillinghast  
; APPLICANT: Drmanac, Radoje T.  
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and  
; TITLE OF INVENTION: Polypeptides  
; FILE REFERENCE: 784CIP2B  
; CURRENT APPLICATION NUMBER: US/09/620,312D  
; CURRENT FILING DATE: 2000-07-19  
; PRIOR APPLICATION NUMBER: 09/552,317  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: 09/488,725  
; PRIOR FILING DATE: 2000-01-21  
; NUMBER OF SEQ ID NOS: 1105  
; SOFTWARE: pt FL Genes Version 1.0  
; SEQ ID NO 777  
; LENGTH: 2521  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (58)..(1653)  
US-09-620-312D-777

Query Match 41.2%; Score 21; DB 4; Length 2521;  
Best Local Similarity 66.7%; Pred. No. 19;  
Matches 30; Conservative 0; Mismatches 15; Indels 0;

QY 6 CACTGCTCTTCTGTGCTTATCCGGCAAGAACTTATCGAAATAC 50  
|||||  
DB 1398 CATGATGCTCTTGTGATTTTCAGGTAAATCTGATGAAATTC 1354  
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RESULT 5  
US-09-453-702B-197/c  
; Sequence 197, Application US/09453702B  
; Patent No. 6365723  
; GENERAL INFORMATION:  
; APPLICANT: Blattner, Frederick R.  
; APPLICANT: Burland, Nicole T.  
; APPLICANT: Plunkett, Guy  
; APPLICANT: Welch, Rod  
; TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157  
; NUMBER OF SEQUENCES: 265  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Charles & Brady  
; STREET: 1 South Pinckney Street  
; CITY: Madison  
; STATE: WI  
; COUNTRY: US  
; ZIP: 53701-2113

APPLICANT: Gary L. Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC99-03PA  
; CURRENT APPLICATION NUMBER: US/09/328,352  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 2457  
; LENGTH: 2553  
; TYPE: DNA  
; ORGANISM: Acinetobacter baumannii  
US-09-328-352-2457

Query Match 40.4%; Score 20.6; DB 4; Length 2553;  
Best Local Similarity 62.7%; Pred. No. 28;  
Matches 32; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 1 GGTACCACTGGTCTTCTGTGCTTATCCGGGCAAGAACTTATCGAAATACA 51  
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Db 336 GGTAAACAGGCTTTGTCATTCATTCGAACGAGTACTTTTAAACAAA 286  
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## RESULT 9

US-09-280-116-134  
; Sequence 134, Application US/09280116A  
; Patent No. 631427  
; GENERAL INFORMATION:  
; APPLICANT: Robison, Keith E.  
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs  
; FILE REFERENCE: 5800-24, 035800/176965  
; CURRENT APPLICATION NUMBER: US/09/280,116A  
; CURRENT FILING DATE: 1999-03-26  
; NUMBER OF SEQ ID NOS: 268  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 134  
; LENGTH: 1000  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: trypsin-like serine proteases  
; NAME/KEY: misc feature  
; LOCATION: (1)..(1000)  
; OTHER INFORMATION: n = a, t, c or g  
US-09-280-116-134

Query Match 40.0%; Score 20.4; DB 4; Length 1000;  
Best Local Similarity 80.0%; Pred. No. 25;  
Matches 24; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 4 ACCACTGGTCTTCTGTGCTTATCCGGGCA 33  
|||||  
Db 223 ACCATTGGTCTTCTGTGCTTATCCGGCA 252  
|||||

## RESULT 10

US-08-785-065-2/c  
; Sequence 2, Application US/08785065  
; Patent No. 581451  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Goli, Surya K.  
; APPLICANT: Hillman, Jennifer L.  
; TITLE OF INVENTION: NOVEL SUBUNITS OF NADH DEHYDROGENASE  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/785,065  
; FILING DATE: Herewith  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0187 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1023 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: Consensus  
; CLONE: Consensus  
US-08-785-065-2

Query Match 39.6%; Score 20.2; DB 1; Length 1023;  
Best Local Similarity 63.3%; Pred. No. 30;  
Matches 31; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 2 GTACCACTGGTCTTCTGTGCTTATCCGGGCAAGAACTTATCGAAATAC 50  
|||||  
Db 383 GCACACCTGAACCTGTGGACATACCTTGGGCAAGATTCAGCCACATAC 335  
|||||

## RESULT 11

US-09-151-412-2/c  
; Sequence 2, Application US/09151412  
; Patent No. 6399345  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Goli, Surya K.  
; APPLICANT: Hillman, Jennifer L.  
; TITLE OF INVENTION: NOVEL SUBUNITS OF NADH DEHYDROGENASE  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA: US/09/151,412  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/785,065  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0187 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166



```
;
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1023 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; IMMEDIATE SOURCE:
;   LIBRARY: Consensus
;   CLONE: Consensus
US-09-151-412-2

Query Match      39.6%; Score 20.2; DB 4; Length 1023;
Best Local Similarity 63.3%; Pred. No. 30;
Matches 31; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 2 GTACCACTGCTCTTCTGCTTATCCGGGCAAGAACTTATCGAAATAC 50
DB 383 GGACACCTGAACCTTGTGGACATACCTTGGGCAAGATTTTCAGCCACATAC 335

RESULT 12
US-09-220-132-5
; Sequence 5, Application US/09220132
; Patent No. 6506607
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT
;   OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 07334-074001
; CURRENT APPLICATION NUMBER: US/09/220,132
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 60/079,303
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: US 60/068,821
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 4775
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-220-132-5

Query Match      39.6%; Score 20.2; DB 4; Length 4775;
Best Local Similarity 75.8%; Pred. No. 52;
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 8 CTGCTCTTCTTGTGCTTATCCGGGCAAGAACTT 40
DB 2647 CTAGCTTGTGTTTCATATAGGGGCAAAAATTT 2679

RESULT 13
US-08-821-994-52
; Sequence 52, Application US/08821994A
; Patent No. 6228643
; GENERAL INFORMATION:
; APPLICANT: Greenland, Andrew J
; APPLICANT: Thomas, Didier RP
; APPLICANT: Jepson, Ian
; TITLE OF INVENTION: Promoters
; FILE REFERENCE: PPD 50108
; CURRENT APPLICATION NUMBER: US/08/821,994A
; PRIOR FILING DATE: 1997-03-22
; EARLIER APPLICATION NUMBER: PCT/GB97/00729
; EARLIER FILING DATE: 1997-03-18
; EARLIER APPLICATION NUMBER: GB 9606062.9
; EARLIER FILING DATE: 1996-03-22
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 675
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; TYPE: DNA
; ORGANISM: Brassica napus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 388, 390, 391, 402, 403, 439..441
; OTHER INFORMATION: n is unknown
US-08-821-994-52

Query Match      39.2%; Score 20; DB 3; Length 675;
Best Local Similarity 65.9%; Pred. No. 32;
Matches 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 2 GTACCACTGCTCTTCTTGTGCTTATCCGGGCAAGAACTTATCGA 45
DB 568 GTACAGGAGAACTCGTATCTTTGTCCGAACAAGAACTTGTGCGA 611

RESULT 14
US-08-821-994-53
; Sequence 53, Application US/08821994A
; Patent No. 6228643
; GENERAL INFORMATION:
; APPLICANT: Greenland, Andrew J
; APPLICANT: Thomas, Didier RP
; APPLICANT: Jepson, Ian
; TITLE OF INVENTION: Promoters
; FILE REFERENCE: PPD 50108
; CURRENT APPLICATION NUMBER: US/08/821,994A
; CURRENT FILING DATE: 1997-03-22
; EARLIER APPLICATION NUMBER: PCT/GB97/00729
; EARLIER FILING DATE: 1997-03-18
; EARLIER APPLICATION NUMBER: GB 9606062.9
; EARLIER FILING DATE: 1996-03-22
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
; LENGTH: 690
; TYPE: DNA
; ORGANISM: Brassica napus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 403, 406, 417..419, 455, 456
; OTHER INFORMATION: n is unknown
US-08-821-994-53

Query Match      39.2%; Score 20; DB 3; Length 690;
Best Local Similarity 65.9%; Pred. No. 32;
Matches 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 2 GTACCACTGCTCTTCTTGTGCTTATCCGGGCAAGAACTTATCGA 45
DB 583 GTACAGGAGAACTCGTATCTTTGTCCGAACAAGAACTTGTGCGA 626

RESULT 15
US-08-899-330-14/c
; Sequence 14, Application US/08899330
; Patent No. 617275
; GENERAL INFORMATION:
; APPLICANT: CORUZZI, GLORIA
; APPLICANT: LAM, HON-MING
; APPLICANT: HSIEH, MING-HSIUN
; TITLE OF INVENTION: PLANT NITROGEN REGULATORY
;   P-II GENES
; TITLE OF INVENTION: P-II GENES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
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Search completed: August 2, 2004, 16:56:31  
Job time : 51 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 2, 2004, 16:14:47 ; Search time 1821 Seconds  
(without alignments)  
836.338 Million cell updates/sec

Title: US-10-068-067-16

Perfect score: 51

Sequence: 1 ggtaccactggtctcttgt.....caagaacttatcgaaataca 51

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Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: em\_estin:\*\*

4: em\_estmu:\*\*

5: em\_estov:\*\*

6: em\_estpl:\*\*

7: em\_estro:\*\*

8: em\_htc:\*\*

9: gb\_est1:\*\*

10: gb\_est2:\*\*

11: gb\_htc:\*\*

12: gb\_est3:\*\*

13: gb\_est4:\*\*

14: gb\_est5:\*\*

15: em\_estfun:\*\*

16: em\_estom:\*\*

17: em\_gss\_hum:\*\*

18: em\_gss\_inv:\*\*

19: em\_gss\_pln:\*\*

20: em\_gss\_vrt:\*\*

21: em\_gss\_fun:\*\*

22: em\_gss\_mam:\*\*

23: em\_gss\_mus:\*\*

24: em\_gss\_pro:\*\*

25: em\_gss\_rcd:\*\*

26: em\_gss\_pbg:\*\*

27: em\_gss\_vrl:\*\*

28: gb\_gss1:\*\*

29: gb\_gss2:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution..

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 4	24.6	48.2	556	9	AV977709

C 5	24.6	48.2	657	9	AV672256
C 6	24.6	48.2	671	13	BW315750
C 7	24.6	48.2	673	29	AG131818
C 8	24.6	48.2	689	13	BW238153
C 9	24.6	48.2	699	9	AV675510
C 10	24.6	48.2	747	28	AZ516237
C 11	24.4	47.8	516	13	BQ988753
C 12	24.4	47.8	639	13	BQ855999
C 13	24.4	47.8	636	13	BQ990860
C 14	24.4	47.8	701	13	BQ855345
C 15	24.4	47.8	711	13	BQ857473
C 16	24.4	47.8	713	13	BQ993947
C 17	24.4	47.8	740	13	BQ847844
C 18	24.4	47.8	741	13	BQ986512
C 19	24.4	47.8	754	13	BQ986671
C 20	24	47.1	258	10	BB646936
C 21	24	47.1	521	13	CA026489
C 22	24	47.1	537	28	BH775634
C 23	24	47.1	545	14	CF370689
C 24	24	47.1	563	14	CF370660
C 25	24	47.1	572	14	CD909873
C 26	24	47.1	574	13	BQ240272
C 27	24	47.1	603	10	BE405787
C 28	24	47.1	607	14	CA732078
C 29	24	47.1	611	14	CA600664
C 30	24	47.1	624	13	BQ465033
C 31	24	47.1	645	13	BQ805758
C 32	24	47.1	667	9	AI725089
C 33	24	47.1	668	13	BQ295372
C 34	24	47.1	689	13	CA013250
C 35	24	47.1	753	14	CD921720
C 36	24	47.1	762	14	CF132850
C 37	24	47.1	887	12	BM816941
C 38	24	47.1	943	12	BI224795
C 39	23.8	46.7	576	28	BH354963
C 40	23.8	46.7	722	12	BM292491
C 41	23.8	46.7	942	28	CC438714
C 42	23.8	46.7	1057	28	CC258247
C 43	23.6	46.3	208	9	AI509242
C 44	23.6	46.3	282	29	CB791444
C 45	23.6	46.3	316	14	CB708794

#### ALIGNMENTS

BI906283 876 bp mRNA linear EST 16-OCT-2001  
LOCUS 603083222F1 NIH\_MGC\_118 Homo sapiens cDNA clone IMAGE:5212541 5',  
DEFINITION mRNA sequence.  
ACCESSION BI906283  
VERSION BI906283.1 GI:16168946  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 876)  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs@mail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM11533 row: k column: 06  
High quality sequence stop: 800.

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FEATURES
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    Location/Qualifiers
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        /db_xref="taxon:9606"
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        /tissue_type="leukocyte"
        /lab_host="DH10B"
        /clone_lib="NIH_MGC 118"
        /notes="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV
        (destroyed); RNA source leukocytes from anonymous pool of
        non-activated adult donors. Library is oligo-dT primed
        and directionally cloned (EcoRV site is destroyed upon
        cloning). Average insert size 1.7 kb, insert size range
        1.2-3.3 kb. Library is normalized and enriched for
        full-length clones and was constructed by C. Gruber
        (Invitrogen). Research Genetics tracking code 027. Note:
        this is a NIH_MGC Library."

ORIGIN
  Query Match      70.6%; Score 36; DB 12; Length 876;
  Best Local Similarity 100.0%; Pred. No. 0.0014;
  Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CTTGTGCTTATCCGGGCAAGAACTTATCGAATACA 51
      |||||
Db 1 CTTGTGCTTATCCGGGCAAGAACTTATCGAATACA 36

RESULT 2
BF568349      1006 bp mRNA linear EST 12-DEC-2000
LOCUS
DEFINITION
  602184537F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300521 5',
  RNA sequence.
ACCESSION
  BF568349
VERSION
  EST.
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
  ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 1006)
  NIH-MGC http://mgc.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Contact: Robert Strausberg, Ph.D.
  Email: cgaabs-r@mail.nih.gov
  Tissue Procurement: ATCC
  CDNA Library Preparation: Ling Hong/Rubin Laboratory
  CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
  DNA Sequencing by: Incyte Genomics, Inc.
  Clone distribution: MGC clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  http://image.llnl.gov
  Plate: LLCMI59 row: j column: 10
  High quality sequence stop: 739.

FEATURES
  source
    1..1006
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="IMAGE:4300521"
      /tissue_type="epithelioid carcinoma cell line"
      /lab_host="DH10B (phage-resistant)"
      /clone_lib="NIH_MGC 42"
      /notes="EcoRI; pancreas; Vector: pOTEB7; Site 1: XhoI;
      Site 2: EcoRI; cDNA made by oligo-dT priming.
      Directionally cloned into EcoRI/XhoI sites using the
      following 5' adaptor: GGCACGAG(G). Size-selected by Ling
      for average insert size 1.8kb. Library constructed by Ling
      Hong in the laboratory of Gerald M. Rubin (University of
      California, Berkeley) using ZAP-cDNA synthesis kit
      (Stratagene) and Superscript II RT (Life Technologies).

Location/Qualifiers
  1..876
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="IMAGE:5212541"
    /tissue_type="leukocyte"
    /lab_host="DH10B"
    /clone_lib="NIH_MGC 118"
    /notes="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV
    (destroyed); RNA source leukocytes from anonymous pool of
    non-activated adult donors. Library is oligo-dT primed
    and directionally cloned (EcoRV site is destroyed upon
    cloning). Average insert size 1.7 kb, insert size range
    1.2-3.3 kb. Library is normalized and enriched for
    full-length clones and was constructed by C. Gruber
    (Invitrogen). Research Genetics tracking code 027. Note:
    this is a NIH_MGC Library."

ORIGIN
  Note: this is a NIH_MGC Library. |"
  Query Match      50.6%; Score 25.8; DB 10; Length 1006;
  Best Local Similarity 81.1%; Pred. No. 20;
  Matches 30; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4 ACCACTGCTCTCTGTTGCTTATCCGGGCAAGAACTT 40
      |||||
Db 705 AAAACTGGTCTCTCTGTTGCTTATCCGGGCAAGAACTT 741

RESULT 3
AV947614/c      461 bp mRNA linear EST 14-MAR-2002
LOCUS
DEFINITION
  AV947614 Nori Satoh unpublished cDNA library, young adult Ciona
  intestinalis cDNA clone ciad01f07 5', mRNA sequence.
ACCESSION
  AV947614
VERSION
  AV947614.1 GI:19425373
KEYWORDS
  EST.
SOURCE
  Ciona intestinalis
  ORGANISM
    Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
    Phlebobranchia; Cionidae; Ciona.
  1 (bases 1 to 461)
  Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
  Expressed genes in Ciona intestinalis
  JOURNAL
    Unpublished (2000)
  COMMENT
    Contact: Nori Satoh
    Department of Zoology
    Kyoto University
    Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
    Tel: 81-75-753-4081
    Fax: 81-75-705-1113
    Email: satoheascidian.zool.kyoto-u.ac.jp.

FEATURES
  source
    1..461
      /organism="Ciona intestinalis"
      /mol_type="mRNA"
      /db_xref="taxon:7719"
      /clone="ciad01f07"
      /tissue_type="whole animal"
      /dev_stage="young adult"
      /clone_lib="Nori Satoh unpublished cDNA library, young
      adult"

ORIGIN
  Query Match      48.2%; Score 24.6; DB 9; Length 461;
  Best Local Similarity 70.2%; Pred. No. 51;
  Matches 33; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 GGTACCACTGCTCTCTGTTGCTTATCCGGGCAAGAACTTATCGAAA 47
      |||||
Db 421 GGTGCCCGCGGCTCTCTGTCATCTTTGGCAAAATGCTTACCGGAA 375

RESULT 4
AV977709/c      556 bp mRNA linear EST 14-MAR-2002
LOCUS
DEFINITION
  AV977709 Nori Satoh unpublished cDNA library, egg Ciona
  intestinalis cDNA clone cie46b20 5', mRNA sequence.
ACCESSION
  AV977709
VERSION
  AV977709.1 GI:19467475
KEYWORDS
  EST.
SOURCE
  Ciona intestinalis
  ORGANISM
    Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
    Phlebobranchia; Cionidae; Ciona.
  1 (bases 1 to 556)
  Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
  Expressed genes in Ciona intestinalis
  JOURNAL
    Unpublished (2000)
  COMMENT
    Contact: Nori Satoh

```

Department of Zoology  
Kyoto University  
Sakyo-Ku, Kyoto, Kyoto 606-8502, Japan  
Tel: 81-75-753-4081  
Fax: 81-75-705-1113  
Email: satcho@ascidian.zool.kyoto-u.ac.jp

FEATURES  
source  
1..556  
/organism="Ciona intestinalis"  
/mol\_type="mRNA"  
/db\_xref="taxon:7719"  
/clone="C1eg46b20"  
/tissue\_type="whole animal"  
/dev\_stage="egg"  
/clone\_lib="Nori Satoh unpublished cDNA library, egg"

ORIGIN  
Query Match 48.2%; Score 24.6; DB 9; Length 556;  
Best Local Similarity 70.2%; Pred. No. 53;  
Matches 33; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
QY 1 GGTACCACTGGTCTTCTTGTGCTTATCCGGCAAGAACTTATCGAAA 47  
|||||  
DB 336 GGTGCGCGGGCTTCTTGTGCTTATCCGGCAAGAACTTATCGAAA 290  
|||||

RESULT 5  
AV672256/c  
LOCUS  
DEFINITION  
AV672256 Nori Satoh unpublished cDNA library Ciona intestinalis  
cDNA clone citb3c5 5', mRNA sequence.  
ACCESSION  
VERSION  
AV672256.1 GI:10110255  
KEYWORDS  
EST.  
SOURCE  
Ciona intestinalis  
ORGANISM  
Ciona intestinalis  
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;  
Phlebobranchia; Cionidae; Ciona.  
1 (bases 1 to 657)  
Satcho, N., Satou, Y., Kohara, Y. and Shin-i, T.  
Expressed genes in Ciona intestinalis  
Unpublished (2000)  
Contact: Nori Satoh  
Department of Zoology  
Kyoto University  
Sakyo-Ku, Kyoto, Kyoto 606-8502, Japan  
Tel: 81-75-753-4081  
Fax: 81-75-705-1113  
Email: satcho@ascidian.zool.kyoto-u.ac.jp.

FEATURES  
source  
1..657  
/organism="Ciona intestinalis"  
/mol\_type="mRNA"  
/db\_xref="taxon:7719"  
/clone="citb3c5"  
/tissue\_type="whole animal"  
/dev\_stage="tailbud"  
/clone\_lib="Nori Satoh unpublished cDNA library"

ORIGIN  
Query Match 48.2%; Score 24.6; DB 9; Length 657;  
Best Local Similarity 70.2%; Pred. No. 55;  
Matches 33; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
QY 1 GGTACCACTGGTCTTCTTGTGCTTATCCGGCAAGAACTTATCGAAA 47  
|||||  
DB 310 GGTGCGCGGGCTTCTTGTGCTTATCCGGCAAGAACTTATCGAAA 264  
|||||

RESULT 6  
BW315750/c  
LOCUS  
DEFINITION  
BW315750 Nori Satoh unpublished cDNA library, heart Ciona  
intestinalis CDNA clone ciht029m20 5', mRNA sequence.

ACCESSION  
VERSION  
BW315750.1 GI:24896434  
KEYWORDS  
EST.  
SOURCE  
Ciona intestinalis  
ORGANISM  
Ciona intestinalis  
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;  
Phlebobranchia; Cionidae; Ciona.  
1 (bases 1 to 671)  
Satou, Y., Shin-i, T., Kohara, Y. and Satcho, N.  
Expressed genes in Ciona intestinalis (2002c)  
Unpublished (2002)  
Contact: Nori Satoh  
Department of Zoology  
Kyoto University  
Sakyo-Ku, Kyoto, Kyoto 606-8502, Japan  
Tel: 81-75-753-4081  
Fax: 81-75-705-1113  
Email: satcho@ascidian.zool.kyoto-u.ac.jp.

FEATURES  
source  
1..671  
/organism="Ciona intestinalis"  
/mol\_type="mRNA"  
/db\_xref="taxon:7719"  
/clone="ciht029m20"  
/tissue\_type="heart"  
/clone\_lib="Nori Satoh unpublished cDNA library, heart"

ORIGIN  
Query Match 48.2%; Score 24.6; DB 13; Length 671;  
Best Local Similarity 70.2%; Pred. No. 55;  
Matches 33; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
QY 1 GGTACCACTGGTCTTCTTGTGCTTATCCGGCAAGAACTTATCGAAA 47  
|||||  
DB 523 GGTGCGCGGGCTTCTTGTGCTTATCCGGCAAGAACTTATCGAAA 477  
|||||

RESULT 7  
AG131818  
LOCUS  
DEFINITION  
AG131818 Pan troglodytes DNA, clone: PTB-144A01.R, genomic survey sequence.  
ACCESSION  
VERSION  
AG131818.1 GI:16661496  
KEYWORDS  
GSS.  
SOURCE  
Pan troglodytes (chimpanzee)  
ORGANISM  
Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
1  
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,  
Totoki, Y., Watanabe, H. and Sakaki, Y.  
BAC end sequences of Library PTB  
Unpublished  
2 (bases 1 to 673)  
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,  
Totoki, Y., Watanabe, H. and Sakaki, Y.  
Direct Submission  
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
(E-mail: chimbes@gsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/;  
Tel: 81-45-503-9111, Fax: 81-45-503-9170)  
Clones are derived from the chimpanzee BAC library PTB This BAC end  
was generated during the R&D process and may have higher chance of  
clone tracking errors.  
PRIMERS  
Sequencing: M13Rev  
LIBRARY  
Vector : pKS145  
R.Site 1 : SacI  
R.Site 2 : SacI.  
Location/Qualifiers

source  
1. .673  
/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
/clone="PTB-144A01.R"  
/sex="male"  
/cell\_type="lymphoblast"  
/clone\_lib="FTB Chimpanzee Male BAC Library"

## ORIGIN

Query Match 48.2%; Score 24.6; DB 29; Length 673;  
Best Local Similarity 70.2%; Pred. No. 55;  
Matches 33; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 4 ACCACTGGTCTTCTTGCTTATCCGGGCAAGAACTTATCGAAATAC 50  
DB 126 ACATCTGCTCTCTTGCTCTCAGCAGCGGAGAGTGATATCAATAC 172

RESULT 8  
BW238153/c

LOCUS BW238153 Nori Satoh unpublished cDNA library, tailbud embryo Ciona  
DEFINITION intestinalis cDNA clone citb058p22 5', mRNA sequence.  
ACCESSION BW238153.1 GI:24760342  
KEYWORDS EST.  
SOURCE Ciona intestinalis

## ORGANISM

Ciona intestinalis  
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;  
Phlebobranchia; Clonidae; Ciona.  
1 (bases 1 to 689)  
Saton, Y., Shin-i, T., Kohara, Y. and Satoh, N.  
Expressed genes in Ciona intestinalis (2002c)  
Unpublished (2002)  
Contact: Nori Satoh  
Department of Zoology  
Kyoto University  
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan  
Tel: 81-75-753-4081  
Fax: 81-75-705-1113  
Email: satoh@ascidian.zool.kyoto-u.ac.jp.

## FEATURES

source  
Location/Qualifiers  
1. .689  
/organism="Ciona intestinalis"  
/mol\_type="mRNA"  
/db\_xref="taxon:7719"  
/clone="citb058p22"  
/tissue\_type="whole animal"  
/dev\_stage="tailbud embryo"  
/clone\_lib="Nori Satoh unpublished cDNA library, tailbud embryo"

## ORIGIN

Query Match 48.2%; Score 24.6; DB 13; Length 689;  
Best Local Similarity 70.2%; Pred. No. 56;  
Matches 33; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 GGTACCACTGGTCTTCTTGCTTATCCGGGCAAGAACTTATCGAAA 47  
DB 294 GGTGCCCGGGTCTTCTTGCTATCTTTGGGCAATGCTACCGGAA 248

RESULT 9  
AV675510/c

LOCUS AV675510 Nori Satoh unpublished cDNA library Ciona intestinalis  
DEFINITION cDNA clone citb12k10 5', mRNA sequence.  
ACCESSION AV675510  
KEYWORDS EST.  
SOURCE Ciona intestinalis

## ORGANISM

Ciona intestinalis  
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;  
Phlebobranchia; Clonidae; Ciona.  
1 (bases 1 to 699)  
Satch, N., Satou, Y., Kohara, Y. and Shin-i, T.  
Expressed genes in Ciona intestinalis  
Unpublished (2000)  
Contact: Nori Satoh  
Department of Zoology  
Kyoto University  
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan  
Tel: 81-75-753-4081  
Fax: 81-75-705-1113  
Email: satoh@ascidian.zool.kyoto-u.ac.jp.

Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;  
Phlebobranchia; Clonidae; Ciona.  
1 (bases 1 to 699)  
Satch, N., Satou, Y., Kohara, Y. and Shin-i, T.  
Expressed genes in Ciona intestinalis  
Unpublished (2000)  
Contact: Nori Satoh  
Department of Zoology  
Kyoto University  
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan  
Tel: 81-75-753-4081  
Fax: 81-75-705-1113  
Email: satoh@ascidian.zool.kyoto-u.ac.jp.

FEATURES  
source

Location/Qualifiers  
1. .699  
/organism="Ciona intestinalis"  
/mol\_type="mRNA"  
/db\_xref="taxon:7719"  
/clone="citb12k10"  
/tissue\_type="whole animal"  
/dev\_stage="tailbud"  
/clone\_lib="Nori Satoh unpublished cDNA library"

## ORIGIN

Query Match 48.2%; Score 24.6; DB 9; Length 699;  
Best Local Similarity 70.2%; Pred. No. 56;  
Matches 33; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 GGTACCACTGGTCTTCTTGCTTATCCGGGCAAGAACTTATCGAAA 47  
DB 391 GGTGCCCGGGTCTTCTTGCTATCTTTGGGCAATGCTACCGGAA 345

RESULT 10  
AZ516237

LOCUS AZ516237 747 bp DNA linear GSS 16-OCT-2000  
DEFINITION RPCI-11-269M6.TJB RPCI-11 Homo sapiens genomic clone RPCI-11-269M6,  
genomic survey sequence.  
ACCESSION AZ516237  
VERSION AZ516237.1 GI:10824441  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 747)  
Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and  
Venter, J.C.  
BAC end sequences of library RPCI-11  
Unpublished (1997)  
Other GSSs: RPCI-11-269M6.TV  
Contact: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: szhao@tigr.org  
Clones are derived from the human BAC library RPCI-11. For BAC  
library availability, please contact Pieter de Jong  
(pieter@dejong.med.buffalo.edu). Clones may be purchased from  
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from  
Research Genet cs (info@resgen.com). BAC end search page:  
http://www.tigr.org/tdb/human/bac\_end\_search/bac\_end\_search.html.  
This BAC end was generated during the R&D process and may have  
higher chance of clone tracking errors.  
Seg primer: SP6  
Class: BAC ends.

FEATURES  
source

Location/Qualifiers  
1. .747  
/organism="Homo sapiens"  
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/db\_xref="GDB:7603205"

/db\_xref="taxon:9606"  
/clone="RPC1-11-269M6"  
/sex="Male"  
/cell\_type="Lymphocytes"  
/clone\_lib="RPC1-11"  
/note="Vector: pBACe3.6; Site\_1: EcoRI; Site\_2: EcoRI;  
RPC111 Human Male BAC Library"

ORIGIN

Query Match 48.2%; Score 24.6; DB 28; Length 747;  
Best Local Similarity 70.2%; Pred.No.56;  
Matches 33; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 4 ACCACTGGTCTTCTGTGCTTATCCGGCCAGAACTTATCGAATAC 50  
|||||  
Db 628 ACATCTGCTCTCCTGTGCTCAGCAGGCGAGGTGATGCAATAC 674  
|||||

RESULT 11  
BQ988753  
LOCUS  
DEFINITION BQ988753 yg.ab1 QG\_EFGHJ lettuce serriola Lactuca sativa cDNA clone  
QGF15M08, mRNA sequence.  
ACCESSION BQ988753  
VERSION BQ988753.1 GI:22408298  
KEYWORDS EST.  
SOURCE Lactuca sativa  
ORGANISM Lactuca sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;  
Cichorieae; Lactuca.  
1 (bases 1 to 516)  
Kozik,A., Micheltore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,  
Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J.,  
Ellison,P., Kolman,J., Slabaugh,M.S., Livingston,K., Zhou,Y.,  
Lai,Z., Church,S., Jackson,L. and Bradford,K.  
Lettuce and Sunflower ESTs from the Compositae Genome Project  
<http://compnomenics.ucdavis.edu/>  
Unpublished (2002)  
Contact: Alexander Kozik [R.W.Micheltore]  
Department of Vegetable Crops, R.W.Micheltore Lab  
University of California at Davis (UCD)  
Amsundson Hall, UCD, Davis, CA 95616, USA  
Tel: 1-(530)-742-1742  
Fax: 1-(530)-752-9659  
Email: akozik@atgc.org [micheltore@vegmail.ucdavis.edu]  
belongs to contig QG\_CA\_Contig4248, see <http://cgdb.ucdavis.edu/>  
for details  
Plate: QGF15 row: M column: 08.  
Location/Qualifiers  
1. 516  
/organism="Lactuca sativa"  
/mol\_type="mRNA"  
/cultivar="L.serriola"  
/db\_xref="taxon:4236"  
/clone="QGF15M08"  
/lab\_host="E.coli"  
/clone\_lib="QG\_EFGHJ lettuce serriola"  
/note="Vector: pBRCNASTAB; the library was constructed  
from 10 different sources of RNA from a single genotype.  
Separate cDNAs were generated using primers that  
incorporated unique 5' and 3' tags to distinguish each  
source of RNA. cDNAs were then pooled, size-fractionated,  
directionally cloned into a custom medium-copy vector and  
transformations made with four size classes to minimize  
size bias. Details of each source of RNA and library  
construction can be obtained at <http://cgdb.ucdavis.edu/>  
TAG TISSUE=flowers post-fertilized  
TAG LIB=QG\_EFGHJ lettuce serriola  
TAG\_SEQ=TCGATCCGG"

FEATURES  
source

```

RESULT 13
BQ990860
LOCUS
DEFINITION BQ990860 696 bp mRNA linear EST 21-AUG-2002
QGF21E21.YG.ab1 QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone
QGF21E21.1 mRNA sequence.
ACCESSION BQ990860
VERSION BQ990860.1 GI:22410395
KEYWORDS EST.
SOURCE Lactuca sativa
ORGANISM Lactuca sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
Cichorieae; Lactuca.
1 (bases 1 to 696)
REFERENCE
AUTHORS Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J.,
Ellison,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y.,
Lai,Z., Church,S., Jackson,L. and Bradford,K.
TITLE Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compgenomics.ucdavis.edu/
JOURNAL Unpublished (2002)
COMMENT Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Amundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
belongs to contig QG_CA_Contig4248, see http://cgdb.ucdavis.edu/
for details.
Plate: QGF21 row: E column: 21.
FEATURES
source
1..696
Location/Qualifiers
/organism="Lactuca sativa"
/mol_type="mRNA"
/cultivar="L. serriola"
/db_xref="taxon:4236"
/clone="QGF21E21"
/lab_host="E.coli"
/clone_lib="QG_EFGHJ lettuce serriola"
/note="Vector: pBRCNASfiAB; The library was constructed
from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgdb.ucdavis.edu/
TAG_TISSUE=flowers post-fertilized
TAG_LIB=QG_EFGHJ lettuce serriola
TAG_SEQ=TCGCATCGG"

ORIGIN
Query Match 47.8%; Score 24.4; DB 13; Length 696;
Best Local Similarity 73.8%; Pred. No. 67;
Matches 31; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 4 ACCACTGGTCTTCTTGCTTATCCGGGCAAGAACTTATCGA 45
|||||
Db 542 AACAAAGGAGTAGTGTCTGTTATCTGAGCAAGAACTTATCGA 583

RESULT 14
BQ855345
LOCUS
DEFINITION BQ855345 701 bp mRNA linear EST 14-AUG-2002
QGB25009.YG.ab1 QG_ABCDI lettuce salinas Lactuca sativa cDNA clone
QGB25009.1 mRNA sequence.
ACCESSION BQ855345
VERSION BQ855345.1 GI:22240810
KEYWORDS EST.
SOURCE Lactuca sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
Cichorieae; Lactuca.
1 (bases 1 to 711)
REFERENCE
AUTHORS Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J.,
Ellison,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y.,
Lai,Z., Church,S., Jackson,L. and Bradford,K.
TITLE Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compgenomics.ucdavis.edu/
JOURNAL Unpublished (2002)
COMMENT Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Amundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
belongs to contig QG_CA_Contig4248, see http://cgdb.ucdavis.edu/
for details.
Plate: QGB25 row: O column: 09.
FEATURES
source
1..701
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/cultivar="Salinas"
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/clone="QGB25009"
/lab_host="E.coli"
/clone_lib="QG_ABCDI lettuce salinas"
/note="Vector: pBRCNASfiAB; The library was constructed
from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgdb.ucdavis.edu/
TAG_TISSUE=flowers post-fertilized
TAG_LIB=QG_ABCDI lettuce salinas
TAG_SEQ=TCGCATCGG"

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Best Local Similarity 73.8%; Pred. No. 67;
Matches 31; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 4 ACCACTGGTCTTCTTGCTTATCCGGGCAAGAACTTATCGA 45
|||||
Db 169 AACAAAGGAGTAGTGTCTGTTATCTGAGCAAGAACTTATCGA 210

RESULT 15
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LOCUS
DEFINITION BQ857473 711 bp mRNA linear EST 14-AUG-2002
QGB7J21.YG.ab1 QG_ABCDI lettuce salinas Lactuca sativa cDNA clone
QGB7J21.1 mRNA sequence.
ACCESSION BQ857473
VERSION BQ857473.1 GI:22242938
KEYWORDS EST.
SOURCE Lactuca sativa
ORGANISM Lactuca sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
Cichorieae; Lactuca.
1 (bases 1 to 711)
REFERENCE
AUTHORS Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J.,
Ellison,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y.,
Lai,Z., Church,S., Jackson,L. and Bradford,K.
TITLE Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compgenomics.ucdavis.edu/
JOURNAL Unpublished (2002)
COMMENT Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Amundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
belongs to contig QG_CA_Contig4248, see http://cgdb.ucdavis.edu/
for details.
Plate: QGB25 row: O column: 09.
FEATURES
source
1..701
Location/Qualifiers
/organism="Lactuca sativa"
/mol_type="mRNA"
/cultivar="Salinas"
/db_xref="taxon:4236"
/clone="QGB25009"
/lab_host="E.coli"
/clone_lib="QG_ABCDI lettuce salinas"
/note="Vector: pBRCNASfiAB; The library was constructed
from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgdb.ucdavis.edu/
TAG_TISSUE=flowers post-fertilized
TAG_LIB=QG_ABCDI lettuce salinas
TAG_SEQ=TCGCATCGG"

ORIGIN
Query Match 47.8%; Score 24.4; DB 13; Length 701;
Best Local Similarity 73.8%; Pred. No. 67;
Matches 31; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 4 ACCACTGGTCTTCTTGCTTATCCGGGCAAGAACTTATCGA 45
|||||
Db 169 AACAAAGGAGTAGTGTCTGTTATCTGAGCAAGAACTTATCGA 210

```



TITLE  
Lai, Z., Church, S., Jackson, L. and Bradford, K.  
Lettuce and Sunflower ESTs from the Compositae Genome Project  
http://compgenomics.ucdavis.edu/  
JOURNAL  
Unpublished (2002)  
COMMENT  
Contact: Alexander Kozik [R.W.Michelmore]  
Department of Vegetable Crops, R.W.Michelmore Lab  
University of California at Davis (UCD)  
Asmundson Hall, UCD Davis, CA 95616, USA  
Tel: 1-(530)-742-1742  
Fax: 1-(530)-752-9659  
Email: akozik@ucdavis.edu [michelmore@vegmail.ucdavis.edu]  
belongs to contig QG\_CA\_Contig4248, see http://cgdb.ucdavis.edu/  
for details.

Plate: QGB7 row: J column: 21.

#### FEATURES

Source

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Location/Qualifiers  
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/db\_xref="taxon:4236"  
/clone="QGB7J21"  
/lab\_host="E.coli"  
/clone\_lib="QG-ABCDI lettuce salinas"  
/note="Vector: pBRCDNASfiAB; The library was constructed  
from 10 different sources of RNA from a single genotype.  
Separate cDNAs were generated using primers that  
incorporated unique 5' and 3' tags to distinguish each  
source of RNA. cDNAs were then pooled, size-fractionated,  
directionally cloned into a custom medium-copy vector and  
transformations made with four size classes to minimize  
size bias. Details of each source of RNA and library  
construction can be obtained at http://cgdb.ucdavis.edu/  
TAG\_TISSUE=flowers post-fertilized  
TAG\_LIB=QG-ABCDI lettuce salinas  
TAG\_SEQ=TCGATCGG"

#### ORIGIN

Query Match 47.8%; Score 24.4; DB 13; Length 711;  
Best Local Similarity 73.8%; Pred. NO. 67;  
Matches 31; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
QY 4 ACCACTGCTCTTCTGTTATCGGCGCAAGAACTTATCGA 45  
Db 294 AACAAAGGAGTTAGTGTCTGTTATCTGAGCAAGAACTTATCGA 335

Search completed: August 2, 2004, 17:27:09  
Job time : 1829 secs

***This Page Blank (uspto)***

U

Score	Match	Length	DB	ID	Description
100	100	100	100	100	100

PS Claim 2; Page 25; 56pp; En  
yy

Claim 2: Page 25: 56pp: English.

CC The present sequence represents a probe for the human CC chemokine  
 CC receptor 3 (CCR3) gene. The probe comprises +10 to +60 of exon 1 of CCR3,  
 CC and is a regulatory sequence for CCR3. CCR3 is expressed on cells  
 CC involved in allergic and/or inflammatory disorders. The gene comprises 4  
 CC exons, with the coding region present on exon 4. The specification  
 CC describes methods of regulating the expression of CCR3. The regulatory  
 CC site is derived from an untranslated exon 1, exon 2, exon 3 or promoter  
 CC of a human CCR3 gene. Regulating the expression of the chemokine receptor  
 CC CCR3 is useful for preventing or treating disorders involving  
 CC eosinophils, such as allergic inflammatory and hypersensitivity  
 CC reactions, certain types of leukemia, and certain infectious disorders  
 CC involving CCR3, e.g. HIV or respiratory syncytial virus infection.  
 CC Expression and modulation of CCR3 is a useful tool in assessing  
 CC eosinophil targeting and in regulating eosinophil-mediated reactions and  
 CC diseases

XX  
 XX  
 SQ Sequence 51 BP; 13 A; 12 C; 11 G; 15 T; 0 U; 0 Other;

Query Match 100.0%; Score 51; DB 6; Length 51;  
 Best Local Similarity 100.0%; Pred. No. 7.9e-12;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACCACTGCTCTTGTGCTTATCCGGGCAAGAACTTATCGAATACA 51  
 Db 1 GGTACCACTGCTCTTGTGCTTATCCGGGCAAGAACTTATCGAATACA 51

## RESULT 2

ABQ78519  
 ID ABQ78519 standard; RNA; 51 BP.

AC ABQ78519;

XX 25-NOV-2002 (first entry)

XX Nucleotide sequence of a regulatory sequence for human CCR3.

XX Human; CC chemokine receptor 3; CCR3; allergic disorder; probe;  
 XX inflammatory disorder; eosinophil; hypersensitivity; leukemia;  
 XX infectious disorder; HIV; respiratory syncytial virus infection; ss.

OS Homo sapiens.

XX WO200262848-A2.

XX 15-AUG-2002.

XX 06-FEB-2002; 2002WO-US003442.

XX 07-FEB-2001; 2001US-0267073P.

XX 05-FEB-2002; 2002US-00068067.

XX (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.

XX Rothenberg ME, Zimmerman N;

XX WPI; 2002-657524/70.

XX New CC chemokine receptor 3 (CCR3) regulatory site in an untranslated  
 FT exon 1, exon 2, exon 3 or promoter of a human CCR3 gene or mRNA capable  
 PT of binding to regulatory elements, useful for preventing e.g. allergic  
 PT inflammatory reactions.

XX Claim 7; Page 56; 56pp; English.

XX The present sequence represents a probe for the human CC chemokine  
 CC receptor 3 (CCR3) gene. The probe is a regulatory sequence for CCR3. CCR3  
 CC is expressed on cells involved in allergic and/or inflammatory disorders.  
 CC The gene comprises 4 exons, with the coding region present on exon 4. The  
 CC specification describes methods of regulating the expression of CCR3. The  
 CC regulatory site is derived from an untranslated exon 1, exon 2, exon 3 or  
 CC promoter of a human CCR3 gene. Regulating the expression of the chemokine  
 CC receptor CCR3 is useful for preventing or treating disorders involving

CC eosinophils, such as allergic inflammatory and hypersensitivity  
 CC reactions, certain types of leukemia, and certain infectious disorders  
 CC involving CCR3, e.g. HIV or respiratory syncytial virus infection.  
 CC Expression and modulation of CCR3 is a useful tool in assessing  
 CC eosinophil targeting and in regulating eosinophil-mediated reactions and  
 CC diseases

SQ Sequence 51 BP; 13 A; 12 C; 11 G; 0 T; 15 U; 0 Other;

Query Match 100.0%; Score 51; DB 6; Length 51;

Best Local Similarity 70.6%; Pred. No. 7.9e-12;

Matches 36; Conservative 15; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACCACTGCTCTTGTGCTTATCCGGGCAAGAACTTATCGAATACA 51  
 Db 1 GGUACCAUGGUGUCUUGUGUUAUCCGGGCAAGAACTTATCGAATACA 51

## RESULT 3

ABQ78513  
 ID ABQ78513 standard; DNA; 2895 BP.

XX AC ABQ78513;

DT 25-NOV-2002 (first entry)

XX Nucleotide sequence of the human CCR3 gene promoter.

XX Human; CC chemokine receptor 3; CCR3; allergic disorder;  
 XX inflammatory disorder; eosinophil; hypersensitivity; leukemia;  
 XX infectious disorder; HIV; respiratory syncytial virus infection;  
 XX promoter; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FT misc\_signal 1640..1645

FT /\*tag= a

FT /note= "splice donor consensus site"

XX WO200262848-A2.

XX 15-AUG-2002.

XX 06-FEB-2002; 2002WO-US003442.

XX 07-FEB-2001; 2001US-0267073P.

XX 05-FEB-2002; 2002US-00068067.

XX (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.

XX Rothenberg ME, Zimmerman N;

XX WPI; 2002-657524/70.

XX New CC chemokine receptor 3 (CCR3) regulatory site in an untranslated  
 FT exon 1, exon 2, exon 3 or promoter of a human CCR3 gene or mRNA capable  
 PT of binding to regulatory elements, useful for preventing e.g. allergic  
 PT inflammatory reactions.

XX Disclosure; Fig 4; 56pp; English.

XX The present sequence represents the promoter of the human CC chemokine  
 CC receptor 3 (CCR3) gene. CCR3 is expressed on cells involved in allergic  
 CC and/or inflammatory disorders. The gene comprises 4 exons, with the  
 CC coding region present on exon 4. The specification describes methods of  
 CC regulating the expression of CCR3. The regulatory site is derived from an  
 CC untranslated exon 1, exon 2, exon 3 or promoter of a human CCR3 gene.  
 CC Regulating the expression of the chemokine receptor CCR3 is useful for  
 CC preventing or treating disorders involving eosinophils, such as allergic  
 CC inflammatory and hypersensitivity reactions, certain types of leukemia,  
 CC and certain infectious disorders involving CCR3, e.g. HIV or respiratory  
 CC syncytial virus infection. Expression and modulation of CCR3 is a useful

CC tool in assessing eosinophil targeting and in regulating eosinophil-mediated reactions and diseases

XX Sequence 2895 BP; 829 A; 590 C; 556 G; 920 T; 0 U; 0 Other;

SQ

Query Match 100.0%; Score 51; DB 6; Length 2895;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-11;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACACATGGTCTTCTTGCTGCTTATCCGGCAAGAACTTATCGAATACA 51  
 |||||  
 Db 1561 GGTACACATGGTCTTCTTGCTGCTTATCCGGCAAGAACTTATCGAATACA 1611

RESULT 4  
 AAT31335  
 ID AAT31335 standard; cDNA; 1193 BP.

XX AAT31335;

XX 15-NOV-1996 (first entry)

XX CC-chemokine receptor 3 cDNA clone.

XX CC-chemokine receptor 3; CXR-3; Eos-L2; inhibitor; antisense;  
 KW antinflammatory; eosinophil; ss.

XX Homo sapiens.

XX Key Location/Qualifiers  
 FH 92..1159  
 FT CDS /\*tag= a

FT variation

FT 918..919 /\*tag= b

FT /note= "CXR-3 cDNA clone has GC at positions 918-919,  
 coding for serine (AGC) at position 276; a genomic clone  
 has CG at these positions, coding for threonine (AGC)"

XX WO9622371-A2.

XX 25-JUL-1996.

XX 19-JAN-1996; 96WO-US000608.

XX 19-JAN-1995; 95US-00375199.

XX (LEUK-) LEUKOSITE INC.

PA (BGM ) BRIGHAM & WOMENS HOSPITAL.

PA (CHIL-) CHILDRENS MEDICAL CENT.

PI Gerard CJ, Gerard NP, Mackay CR, Ponath PD, Post TW, Qin S;

DR WPI; 1996-354528/35.

DR P-PSDB; AAW03377.

XX Mammalian chemokine receptor-3 and related nucleic acids - useful to  
 PT identify receptor inhibitors to treat inflammatory disease, e.g.  
 PT autoimmune disorders, certain cancers, etc.

XX Claim 1; Page 111-113; 153pp; English.

XX A genomic DNA clone (AAT31335) codes for a novel receptor (AAW03377),  
 CC designated Eos L2 or C-C chemokine receptor 3 (CXR-3), involved in  
 CC leukocyte migration associated with inflammation. It was isolated from a  
 CC human library constructed from eosinophils obtd. from a patient with  
 CC hyper-eosinophilic syndrome using a probe (p4 cDNA) encoding the MIP-  
 CC alpha/RANTES receptor. A CXR-3 genomic clone (AAT31334) was also  
 CC isolated, and a consensus sequence is given in AAT31336. The cDNA and  
 CC genomic clones can be used for the prodn. of recombinant CXR-3 in host  
 CC cells, or to design antisense sequences useful for treating inflammatory  
 CC disease

XX Sequence 1193 BP; 274 A; 310 C; 275 G; 334 T; 0 U; 0 Other;

Query Match 68.6%; Score 35; DB 2; Length 1193;  
 Best Local Similarity 100.0%; Pred. No. 0.00013;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TTGTGCTTATCCGGCAAGAACTTATCGAATACA 51  
 |||||  
 Db 1 TTGTGCTTATCCGGCAAGAACTTATCGAATACA 35

RESULT 5  
 AAV07403  
 ID AAV07403 standard; cDNA; 1193 BP.

XX AAV07403;

XX 28-SEP-1998 (first entry)

XX Human C-C chemokine receptor 3 cDNA.

XX C-C chemokine receptor 3; CXR-3; CCR3; Eos L2; human;  
 KW G protein-coupled receptor; leukocyte; antibody; antagonist;  
 KW inflammation; allergy; asthma; graft rejection; infection;  
 KW autoimmune disease; drug screening; therapy; ds.

XX Homo sapiens.

XX Key Location/Qualifiers  
 FH 92..1159  
 FT CDS /\*tag= a

XX WO9814480-A1.

XX 09-APR-1998.

XX 24-SEP-1997; 97WO-US017103.

XX 30-SEP-1996; 96US-00720565.

XX (LEUK-) LEUKOSITE INC.

XX Mackay CR, Ponath PD;

XX WPI; 1998-286418/25.

XX P-PSDB; AAW51745.

XX Antibodies to chemokine receptor-3 protein - useful for diagnosis and  
 PT treatment of inflammatory conditions, e.g. allergy, asthma, autoimmune  
 PT disease, graft rejection or cancer.

XX Example 8; Page 134-136; 185pp; English.

XX This cDNA codes for novel human C-C chemokine receptor 3 (see AAW51745),  
 CC also designated CXR-3, CCR3 or Eos L2, that binds and mediates chemotaxis  
 CC in response to chemokines such as eotaxin, RANTES and MCP-3. The cDNA was  
 CC isolated from a human eosinophil cDNA library constructed from  
 CC eosinophils obtained from a patient with hypereosinophilic syndrome, and  
 CC using CXR-1 cDNA as probe. A genomic DNA sequence (see AAV07402) is also  
 CC provided as well as a consensus sequence (see AAV07404) for CXR-3. The  
 CC invention relates to isolated and/or recombinant nucleic acids encoding  
 CC CXR-3, isolated or recombinant CXR-3 polypeptides, recombinant CXR-3  
 CC acid constructs, host cells useful for production of recombinant CXR-3  
 CC proteins, to antibodies reactive with the receptors, and to methods of  
 CC using these products to identify ligands, antagonists and agonists of  
 CC receptor function. Inhibitors of CXR-3 can be used to treat: inflammatory  
 CC or allergic diseases and conditions, including respiratory allergic  
 CC diseases such as asthma, allergic rhinitis, hypersensitivity lung  
 CC disease, hypersensitivity pneumonitis, eosinophilic pneumonia (e.g.  
 CC Loeffler's syndrome, chronic eosinophilic pneumonia, interstitial lung  
 CC disease [ILD] e.g. idiopathic pulmonary fibrosis or ILD associated with  
 CC rheumatoid arthritis, systemic lupus erythematosus, ankylosing  
 CC spondylitis, systemic sclerosis, Sjogren's syndrome, polymyositis or  
 CC dermatomyositis), systemic anaphylaxis or hypersensitivity responses,

CC drug allergy, insect sting allergy, inflammatory bowel disease, such as  
 CC Crohn's disease and ulcerative colitis, spondyloarthritis, scleroderma,  
 CC psoriasis, inflammatory dermatosis such as dermatitis, eczema, atopic  
 CC dermatitis, allergic contact dermatitis, urticaria, vasculitis (e.g.  
 CC necrotizing, cutaneous and hypersensitivity vasculitis); eosinophilic  
 CC myositis and eosinophilic fasciitis; autoimmune diseases such as  
 CC rheumatoid arthritis, psoriatic arthritis, multiple sclerosis, systemic  
 CC lupus erythematosus, myasthenia gravis, juvenile onset diabetes,  
 CC glomerulonephritis, autoimmune thyroiditis and Behcet's disease; graft  
 CC rejection, including allograft rejection or graft-versus-host disease;  
 CC cancers with leukocyte infiltration of the skin or organs; and also  
 CC reperfusion injury, atherosclerosis, certain haematologic malignancies,  
 CC septic shock and endotoxic shock. Promoters of CKR-3 function can be used  
 CC for treating: immunosuppression e.g. in AIDS patients or individuals  
 CC undergoing radiation therapy, chemotherapy, therapy for autoimmune  
 CC disease or other drug therapy, and immunosuppression due congenital  
 CC deficiency in receptor function or other causes; and infectious diseases  
 CC such as parasitic diseases, including helminth infections, such as  
 CC nematodes (round worms). The agents can also be used for detection and  
 CC diagnosis  
 CC  
 SQ Sequence 1193 BP; 274 A; 310 C; 275 G; 334 T; 0 U; 0 Other;

Query Match 68.6%; Score 35; DB 2; Length 1193;

Best Local Similarity 100.0%; Pred. No. 0.00013;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TTGTGCTTATCCGGCAAGAACTTATCGAATACA 51

DB 1 TTGTGCTTATCCGGCAAGAACTTATCGAATACA 35

RESULT 6

ADA20738

ID ADA20738 standard; cDNA; 1342 BP.

XX AC ADA20738;

XX DT 20-NOV-2003 (first entry)

XX DE Wheat cDNA encoding a cytosine 5-methyltransferase #1.

XX KW ss; gene; plant; respiratory burst oxidase; Rboh; trna-mnm-s-U-MT;

XX KW chromomethylase; cytosine 5-methyltransferase; phospholipase D;

XX KW transcription factor IIF; asparaginyl tRNA transferase;

XX KW glutaminyl tRNA transferase; EDS1; adaptin AP50; adaptin alpha;

XX KW adaptin betas; stress resistance; quality grain improvement; starch;

XX KW herbicide.

OS Triticum aestivum.

XX US2003003471-A1.

XX PD 02-JAN-2003.

XX PF 19-FEB-2002; 2002US-00078770.

XX PR 12-JUL-1999; 99US-0143400P.

XX PR 12-JUL-1999; 99US-0143405P.

XX PR 12-JUL-1999; 99US-0143410P.

XX PR 13-SEP-1999; 99US-0153534P.

XX PR 01-OCT-1999; 99US-0157401P.

XX PR 15-OCT-1999; 99US-0159878P.

XX PR 22-OCT-1999; 99US-0161223P.

XX PR 11-JUL-2000; 2000US-00614188.

XX PA (FAMO/) FAMODU O O.

XX PA (MIAO/) MIAO G.

XX PA (SIMM/) SIMMONS C R.

XX PA (WENG/) WENG Z.

XX PA (CAHO/) CAHOON R E.

XX PA (SAKA/) SAKAI H.

XX PA (QUNZ/) QUN Z.

(THOR/) THORPE C J.

PA (FADE/) FADER G M.

XX (LIBB/) LI B.

PI Fancdu OO, Miao G, Simmons CR, Weng Z, Cahoon RE, Sakai H;

PI Qun Z, Thorpe CU, Fader GM, Li B;

XX WPI; 2003-311885/30.

DR P-PSDB; ADA20739.

XX New phospholipase D polypeptides and polynucleotides, useful for  
 PT genetically and physically mapping the genes that they are part of, and  
 PT subsequently in plant breeding for developing lines with the desired  
 PT phenotypes.

PS Disclosure; Page 110; 189pp; English.

XX The invention relates to an isolated polynucleotide encoding a  
 CC phospholipase D comprising a nucleotide sequence (encoding a polypeptide  
 CC of at least 80 amino acids having at least 92% identity based on the  
 CC Clustal method of alignment when compared to the proteins appearing as ID  
 CC 120-134 (even numbers) or their complements. Also included are  
 CC nucleotides encoding 98 plant proteins (comprising respiratory burst  
 CC oxidases (Rboh), trna-mnm-s-U-MT, chromomethylases, cytosine 5-  
 CC methyltransferases, phospholipase D, transcription factor IIF,  
 CC asparaginyl tRNA transferases, glutaminyl tRNA transferases, EDS1 (not  
 CC defined), adaptin AP50, adaptin alpha and adaptin betas), chimaeric  
 CC genes, host cells comprising the chimaeras, a virus comprising the gene,  
 CC the encoded phospholipase D proteins, a method of selecting an isolated  
 CC polynucleotide that affects the level of expression of a phospholipase D  
 CC polypeptide in a plant cell, a method of obtaining a nucleic acid  
 CC fragment encoding a phospholipase D polypeptide, a method for positive  
 CC selection of a transformed cell and a method of altering the level of  
 CC expression of a phospholipase D in a host cell. The polynucleotides may  
 CC be used as probes for genetically and physically mapping the genes that  
 CC they are part of, and as markers for traits linked to those genes. Such  
 CC information may be used in plant breeding to develop lines with the  
 CC desired phenotypes. The nucleic acids are useful in creating transgenic  
 CC plants in which the polypeptides are present at higher or lower levels  
 CC than normal, in cell types or developmental stages in which they are not  
 CC normally found, and which would alter the level of stress and disease  
 CC resistance, enhancement of gene expression or transcription, quality  
 CC grain improvement, or generation of novel starches in those cells. The  
 CC polypeptides can be used as a target to facilitate design and/or  
 CC identification of inhibitors of those enzymes that may be useful as  
 CC herbicides. The present sequence is a cDNA encoding one of the 98  
 CC proteins of the invention.

XX SQ Sequence 1342 BP; 351 A; 281 C; 340 G; 370 T; 0 U; 0 Other;

Query Match

Best Local Similarity 43.9%; Score 22.4; DB 7; Length 1342;

Matches 32; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 4 ACCACTGCTCTTCTTGCTTATCCGGCAAGAACTTATCGAATACA 51

DB 352 AGCACTGCTGTTGGGCGCCCTTCCTCGCAATAAATCTGTAGATACA 399

RESULT 7

ADA20746

ID ADA20746 standard; cDNA; 1343 BP.

XX AC ADA20746;

XX DT 20-NOV-2003 (first entry)

XX DE Wheat cDNA encoding a cytosine 5-methyltransferase #3.

XX KW ss; gene; plant; respiratory burst oxidase; Rboh; trna-mnm-s-U-MT;

XX KW chromomethylase; cytosine 5-methyltransferase; phospholipase D;

XX KW transcription factor IIF; asparaginyl tRNA transferase;

XX KW glutaminyl tRNA transferase; EDS1; adaptin AP50; adaptin alpha;

KW adaptin betas; stress resistance; quality grain improvement; starch;  
KW herbicide.  
XX  
OS Tricum aestivum.  
XX  
PN US2003003471-A1.  
XX  
XX 02-JAN-2003.  
XX  
XX 19-FEB-2002; 2002US-00078770.  
XX  
PR 12-JUL-1999; 99US-0143400P.  
PR 12-JUL-1999; 99US-0143409P.  
PR 12-JUL-1999; 99US-0143410P.  
PR 13-SEP-1999; 99US-0153534P.  
PR 01-OCT-1999; 99US-0157401P.  
PR 15-OCT-1999; 99US-0159878P.  
PR 22-OCT-1999; 99US-0161223P.  
PR 11-JUL-2000; 2000US-00614188.  
XX  
XX (FAMO/) FAMODU O O.  
PA (MIAO/) MIAO G.  
PA (SIMW/) SIMMONS C R.  
PA (WENG/) WENG Z.  
PA (CAHO/) CAHOON R E.  
PA (SAXA/) SAKAI H.  
PA (QUNZ/) QUN Z.  
PA (THOR/) THORPE C J.  
PA (FADE/) FADER G M.  
PA (LIBB/) LI B.  
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PI Qun Z, Thorpe CJ, Fader GW, Li B;  
PI  
DR WPI; 2003-311885/30.  
DR P-PSDB; ADA20747.  
XX  
XX New phospholipase D polypeptides and polynucleotides, useful for  
PT genetically and physically mapping the genes that they are part of, and  
PT subsequently in plant breeding for developing lines with the desired  
PT phenotypes.  
XX  
PS Disclosure; Page 115-116; 189pp; English.  
XX  
XX The invention relates to an isolated polynucleotide encoding a  
CC phospholipase D comprising a nucleotide sequence (encoding a polypeptide  
CC of at least 80 amino acids having at least 92% identity based on the  
CC Clustal method of alignment when compared to the proteins appearing as ID  
CC 120-134 (even numbers) or their complements. Also included are  
CC nucleotides encoding 98 plant proteins (comprising respiratory burst  
CC oxidases (Rboh), TRNA-mmm-8-U-MT, chromomethylases, cytosine 5-  
CC methyltransferases, phospholipase D, transcription factor Ilr,  
CC asparaginyl tRNA transferases, glutamyl tRNA transferases, EDS1 (not  
CC defined), adaptin AP50, adaptin alphas and adaptin betas), chimaeric  
CC genes, host cells comprising the chimaeras, a virus comprising the gene,  
CC the encoded phospholipase D proteins, a method of selecting an isolated  
CC polynucleotide that affects the level of expression of a phospholipase D  
CC polypeptide in a plant cell, a method of obtaining a nucleic acid  
CC fragment encoding a phospholipase D polypeptide, a method for positive  
CC selection of a transformed cell and a method of altering the level of  
CC expression of a phospholipase D in a host cell. The polynucleotides may  
CC be used as probes for genetically and physically mapping the genes that  
CC they are part of, and as markers for traits linked to those genes. Such  
CC information may be used in plant breeding to develop lines with the  
CC desired phenotypes. The nucleic acids are useful in creating transgenic  
CC plants in which the polypeptides are present at higher or lower levels  
CC than normal, in cell types or developmental stages in which they are not  
CC normally found, and which would alter the level of stress and disease  
CC resistance, enhancement of gene expression or transcription, quality  
CC grain improvement, or generation of novel starches in those cells. The  
CC polypeptides can be used as a target to facilitate design and/or  
CC identification of inhibitors of those enzymes that may be useful as  
CC herbicides. The present sequence is a cDNA encoding one of the 98

CC proteins of the invention.  
XX  
SQ Sequence 1343 BP; 351 A; 281 C; 340 G; 371 T; 0 U; 0 Other;  
Query Match 43.9%; Score 22.4; DB 7; Length 1343;  
Best Local Similarity 66.7%; Pred. No. 34;  
Matches 32; Conservative 0; Mismatches 16; Indels 0; Gaps 0;  
Qy 4 ACCACTGGTCTTCTTGTGCTTATCCGGGCGAGAACTATCGAATACA 51  
Db 352 AGCACTGCTGGTGGGCGCCTTTCCGTCGCAATACTGTTAGAGATACA 399  
RESULT 8  
AAH30283  
ID AAH30283 standard; cDNA; 420 BP.  
XX  
AC AAH30283;  
XX  
XX 27-JUL-2001 (first entry)  
XX  
XX Human colon cancer cell line Kml2L4-A cDNA library derived sequence #217.  
XX  
KW Human; diagnosis; colon cancer; cancer; malignant; chromosome mapping;  
KW detection; colon cancer cell line Kml2L4-A; ss.  
XX  
OS Homo sapiens.  
XX  
XX WO200018916-A2.  
XX  
XX 06-APR-2000.  
XX  
XX 23-SEP-1999; 99WO-US022226.  
XX  
XX 28-SEP-1998; 98US-0102161P.  
XX 28-SEP-1998; 98US-0102180P.  
XX 29-SEP-1998; 98US-0102380P.  
XX 08-OCT-1998; 98US-0103815P.  
XX 27-OCT-1998; 98US-0105877P.  
XX  
XX (CHIR ) CHIRON CORP.  
XX (HYSE-) HYSEQ INC.  
XX  
XX Williams LT, Escobedo J, Innis MA, Garcia PD, Sudduth-Klinger J;  
PI Reinhard C, Giese K, Randazzo F, Kennedy GC, Pot D, Kassam A;  
PI Lamson G, Drmanac R, Crkvenjakov R, Dickson M, Drmanac S, Labat I;  
PI Leshkowitz D, Kita D, Garcia V, Jones LW, Stache-Crain B;  
XX  
XX WPI; 2000-293155/25.  
XX  
XX Polynucleotide library comprising 1079 defined sequences, useful in the  
XX form of an array to detect cancer or susceptibility to cancer.  
XX  
XX Claim 1; Page 246; 502pp; English.  
XX  
XX The present invention describes a library of polynucleotides comprising  
CC 1079 nucleotide sequences (given in AAH30067 to AAH31145). Also described  
CC are: (1) an isolated polynucleotide (I) having at least 90% identity to  
CC one of the 1079 sequences; (2) a recombinant host cell containing (I);  
CC (3) an isolated polypeptide (II) encoded by (I); (4) an antibody that  
CC specifically binds to (II); (5) a vector comprising (I); and (6) a method  
CC of detecting differentially expressed genes correlated with a cancerous  
CC state of a mammalian cell comprising detecting a gene product encoded by  
CC one of the 1079 sequences given in the specification. The polynucleotides  
CC are used to monitor patients having (or susceptible) to cancer to detect  
CC potentially malignant events at a molecular level before they are  
CC detectable at a gross morphological level. The polynucleotides are also  
CC useful for monitoring the efficacy of various therapies and preventive  
CC interventions. Polynucleotide probes based on the disclosed sequences are  
CC useful for chromosome mapping and detection of transcription levels. The  
CC 1079 polynucleotide sequences were derived from a human colon cancer cell  
CC line Kml2L4-A cDNA library  
XX

SQ Sequence 420 BP; 113 A; 113 C; 100 G; 93 T; 0 U; 1 Other;  
 Query Match 43.5%; Score 22.2; DB 3; Length 420;  
 Best Local Similarity 77.1%; Pred. No. 30;  
 Matches 27; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
 QY 5 CCACGTGCTCTTGTGCTTATCCGGCAAGAACT 39  
 ||| ||||| ||| ||| ||||| |||||  
 Db 207 CCACGGCTCTTCTCTCTCTCTCCCAAGAACT 241

RESULT 9  
 AAF74867  
 ID AAF74867 standard; DNA; 1313 BP.  
 AC AAF74867;

XX 22-MAY-2001 (first entry)  
 XX Leishmania major PPG nucleotide sequence.  
 XX Human; hPPG-1; PPG; proteophosphoglycan; detection; ds.  
 XX Leishmania major.  
 XX CN1272542-A.  
 XX 08-NOV-2000.  
 XX 11-APR-2000; 2000CN-00115368.  
 XX 11-APR-2000; 2000CN-00115368.  
 XX (NANF-) NANFANG RES CENT STATE HUMAN GENE GROUP.  
 XX Li N, Xiao H, Kang B;  
 XX WPI; 2001-183595/19.  
 XX P-PSDB; AAB74609.  
 XX Human phosphoglycan protein and its coded sequence.  
 XX Example 2; Page 17-19; 22pp; Chinese.

XX The present invention describes a human proteophosphoglycan protein designated hPPG-1. Also describes are methods for the preparation and detection of hPPG-1. The present sequence encodes the Leishmania major PPG protein which is used in comparison with the hPPG-1 protein, in an example from the present invention  
 XX Sequence 1313 BP; 194 A; 457 C; 367 G; 295 T; 0 U; 0 Other;  
 Query Match 43.5%; Score 22.2; DB 4; Length 1313;  
 Best Local Similarity 59.8%; Pred. No. 41;  
 Matches 30; Conservative 0; Mismatches 13; Indels 0; Gaps 0;  
 QY 4 ACCACTGCTCTTGTGCTTATCCGGCAAGAACTATCGAA 46  
 ||| ||||| ||| ||| ||||| |||||  
 Db 878 ACCACAGCACTTCTGTGGTGATATATCAAGAACTACTCGAA 920

RESULT 10  
 ABK73357  
 ID ABK73357 standard; DNA; 1719 BP.  
 AC ABK73357;  
 XX 13-AUG-2002 (first entry)

XX Bacillus licheniformis genomic sequence tag (GST) #648.  
 XX Differential gene expression; genomic sequenced tag; GST;  
 XX altered culture condition; environmental stress;  
 KW

KW physiological provocation; ds.  
 XX Bacillus licheniformis.  
 XX WO200229113-A2.  
 XX 11-APR-2002.  
 XX 05-OCT-2001; 2001WO-US031437.  
 XX 06-OCT-2000; 2000US-00680598.  
 XX 27-MAR-2001; 2001US-0279526P.  
 XX (NOVO) NOVOZYMES BIOTECH INC.  
 XX (NOVO) NOVOZYMES AS.  
 XX Berka R, Clausen IG;  
 XX WPI; 2002-416684/44.  
 XX Monitoring differential expression of several genes in first Bacillus cell relative to expression of same genes in one or more second Bacillus cells, by using substrate containing Bacillus genomic sequenced tag array.  
 XX Claim 4; SEQ ID NO 648; 200pp; English.

XX The invention describes a method of monitoring differential expression of genes in a first Bacillus cell relative to expression of the genes in other Bacillus cells, comprising hybridising labelled nucleic acid probes isolated from Bacillus cells to a substrate containing array of Bacillus genomic sequenced tags (GST), examining the array, and determining relative gene expression by an observed hybridisation reporter signal of a spot in the array. The method is useful for measuring the expression of genes in a first Bacillus cell relative to expression of the same genes in one or more second Bacillus cells. The method is useful for monitoring global expression of several genes from a Bacillus cell, discovering new genes, identifying possible functions of unknown open reading frames and monitoring gene copy number variation and stability. Monitoring changes in expression of genes may be used to provide a representation of the way in which Bacillus cells adapt to changes in culture conditions. Extensive follow up characterisation is unnecessary, when one spot on an array equals one gene or one open reading frame, since sequence information is available. This sequence represents a genomic sequence tag (GST) used in the method of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pat\_sequences  
 XX Sequence 1719 BP; 530 A; 375 C; 413 G; 401 T; 0 U; 0 Other;

Query Match 43.5%; Score 22.2; DB 6; Length 1719;  
 Best Local Similarity 77.1%; Pred. No. 44;  
 Matches 27; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
 QY 13 CTTCTTGCTTATCCGGCAAGAACTATCGAAA 47  
 ||| ||||| ||| ||| ||||| |||||  
 Db 1120 CTTCTGCTGCTCTCGGCAAGTACATATCGAAA 1154

RESULT 11  
 AAS62217  
 ID AAS62217 standard; cDNA; 1861 BP.  
 XX AC  
 XX AAS62217;  
 XX 14-FEB-2002 (first entry)

XX cDNA sequence #4 encoding novel human secreted protein.  
 XX Human secreted protein; hyperproliferative disorder; autoimmune disorder;  
 KW immune deficiency disorder; blood disorder; inflammatory disorder;  
 KW infectious disorder; gene therapy; antimicrobial; hepatotropic;  
 KW





PR 27-SEP-2000; 2000US-0235836P.  
 PR 29-SEP-2000; 2000US-0236327P.  
 PR 29-SEP-2000; 2000US-0236367P.  
 PR 29-SEP-2000; 2000US-0236368P.  
 PR 29-SEP-2000; 2000US-0236369P.  
 PR 29-SEP-2000; 2000US-0236370P.  
 PR 02-OCT-2000; 2000US-0236802P.  
 PR 02-OCT-2000; 2000US-0237037P.  
 PR 02-OCT-2000; 2000US-0237038P.  
 PR 02-OCT-2000; 2000US-0237039P.  
 PR 02-OCT-2000; 2000US-0237040P.  
 PR 13-OCT-2000; 2000US-0239935P.  
 PR 13-OCT-2000; 2000US-0239937P.  
 PR 20-OCT-2000; 2000US-0240960P.  
 PR 20-OCT-2000; 2000US-0241221P.  
 PR 20-OCT-2000; 2000US-0241785P.  
 PR 20-OCT-2000; 2000US-0241786P.  
 PR 20-OCT-2000; 2000US-0241787P.  
 PR 20-OCT-2000; 2000US-0241808P.  
 PR 20-OCT-2000; 2000US-0241809P.  
 PR 01-NOV-2000; 2000US-0241826P.  
 PR 08-NOV-2000; 2000US-0244617P.  
 PR 08-NOV-2000; 2000US-0246474P.  
 PR 08-NOV-2000; 2000US-0246475P.  
 PR 08-NOV-2000; 2000US-0246476P.  
 PR 08-NOV-2000; 2000US-0246477P.  
 PR 08-NOV-2000; 2000US-0246478P.  
 PR 08-NOV-2000; 2000US-0246523P.  
 PR 08-NOV-2000; 2000US-0246524P.  
 PR 08-NOV-2000; 2000US-0246525P.  
 PR 08-NOV-2000; 2000US-0246526P.  
 PR 08-NOV-2000; 2000US-0246527P.  
 PR 08-NOV-2000; 2000US-0246528P.  
 PR 08-NOV-2000; 2000US-0246532P.  
 PR 08-NOV-2000; 2000US-0246609P.  
 PR 08-NOV-2000; 2000US-0246610P.  
 PR 08-NOV-2000; 2000US-0246611P.  
 PR 08-NOV-2000; 2000US-0246613P.  
 PR 17-NOV-2000; 2000US-0249207P.  
 PR 17-NOV-2000; 2000US-0249208P.  
 PR 17-NOV-2000; 2000US-0249209P.  
 PR 17-NOV-2000; 2000US-0249210P.  
 PR 17-NOV-2000; 2000US-0249211P.  
 PR 17-NOV-2000; 2000US-0249212P.  
 PR 17-NOV-2000; 2000US-0249213P.  
 PR 17-NOV-2000; 2000US-0249214P.  
 PR 17-NOV-2000; 2000US-0249215P.  
 PR 17-NOV-2000; 2000US-0249216P.  
 PR 17-NOV-2000; 2000US-0249217P.  
 PR 17-NOV-2000; 2000US-0249218P.  
 PR 17-NOV-2000; 2000US-0249244P.  
 PR 17-NOV-2000; 2000US-0249245P.  
 PR 17-NOV-2000; 2000US-0249246P.  
 PR 17-NOV-2000; 2000US-0249249P.  
 PR 17-NOV-2000; 2000US-0249257P.  
 PR 17-NOV-2000; 2000US-0249299P.  
 PR 01-DEC-2000; 2000US-0249300P.  
 PR 01-DEC-2000; 2000US-0250160P.  
 PR 01-DEC-2000; 2000US-0250391P.  
 PR 05-DEC-2000; 2000US-0251030P.  
 PR 05-DEC-2000; 2000US-0251988P.  
 PR 05-DEC-2000; 2000US-0256719P.  
 PR 06-DEC-2000; 2000US-0251479P.  
 PR 08-DEC-2000; 2000US-0251856P.  
 PR 08-DEC-2000; 2000US-0251868P.  
 PR 08-DEC-2000; 2000US-0251869P.  
 PR 08-DEC-2000; 2000US-0251899P.  
 PR 08-DEC-2000; 2000US-0251990P.  
 PR 11-DEC-2000; 2000US-0254097P.  
 PR 05-JAN-2001; 2001US-0259678P.  
 (HUMA-) HUMAN GENOME SCI INC.  
 PA XX  
 XX  
 PI Rosen CA, Barash SC, Ruben SM;  
 XX WPI; 2001-488783/53.  
 DR P-F5DB; AAU16102.  
 XX  
 PT New nucleic acid molecules encoding 461 human secreted proteins for  
 PT diagnosing, preventing, treating or ameliorating medical conditions and  
 PT used as food additives or preservatives.  
 XX  
 PS Claim 1; SEQ ID NO 268; 980pp; English.  
 XX  
 CC The invention relates to isolated nucleic acid molecules and their  
 CC encoded secreted proteins. The nucleic acids and proteins are used to  
 CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,  
 CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used  
 CC in diagnosing a pathological condition or susceptibility to a  
 CC pathological condition. Antibodies to the proteins can also be used in  
 CC alleviating symptoms associated with the disorders and in diagnostic  
 CC immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays  
 CC (ELISA). Disorders which are diagnosed or treated include autoimmune  
 CC diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g.  
 CC neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac  
 CC arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiodenesis,  
 CC nervous system disorders e.g. Alzheimer's disease, infections caused by  
 CC bacteria, viruses and fungi and ocular disorders e.g. corneal infection,  
 CC and many other disorders listed in the specification. The polypeptides  
 CC can also be used to aid wound healing and epithelial cell proliferation,  
 CC to prevent skin aging due to sunburn, to maintain organs before  
 CC transplantation, for supporting cell culture of primary tissues, to  
 CC regenerate tissues and in chemotaxis. The polypeptides can also be used  
 CC as a food additive or preservative to increase or decrease storage  
 CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,  
 CC minerals, cofactors and other nutritional components. The present  
 CC sequence encodes a novel secreted protein of the invention. Note: The  
 CC sequence data for this patent did not form part of the printed  
 Query Match 43.5%; Score 22.2; DB 4; Length 2102;  
 Best Local Similarity 77.1%; Pred. No. 46;  
 Matches 27; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
 QY 5 CCACGGCTCTTCTGCTTATCCGGCGCAAGAACT 39  
 |||||  
 Db 1104 CCACGGCTCTTCTCTCTCTCTCCAGCAAGAACT 1138  
 |||||  
 RESULT 13  
 ABX73430  
 ID ABX73430 standard; DNA; 2102 BP.  
 XX  
 AC ABX73430;  
 XX  
 DT 18-MAR-2003 (first entry)  
 XX  
 DE Human novel polynucleotide #258.  
 XX  
 KW Human; gene; ds; neural disorder; immune system disorder; renal disorder;  
 KW muscular disorder; respiratory disease; reproductive disorder;  
 KW gastrointestinal disorder; pulmonary disorder; cardiovascular disorder;  
 KW hyperproliferative disorder; inflammatory disease; allergic reaction;  
 KW blood related disorder; cancer; immunosuppressive; antiinflammatory;  
 KW cardiovascular; nephrotropic; cytostatic; antiallergic; thrombolytic;  
 KW haemostatic; antiarteriosclerotic.  
 XX  
 OS Homo sapiens.  
 XX  
 XX US2002132753-A1.  
 PN  
 XX  
 PD 19-SEP-2002.  
 XX  
 PF 17-JAN-2001; 2001US-00764864.  
 PR 31-JAN-2000; 2000US-0179065P.  
 PR 04-FEB-2000; 2000US-0180628P.  
 PR

PR 28-JUN-2000; 2000US-0214886P.  
PR 07-JUL-2000; 2000US-0216647P.  
PR 07-JUL-2000; 2000US-0216880P.  
PR 11-JUL-2000; 2000US-0217487P.  
PR 11-JUL-2000; 2000US-0217496P.  
PR 14-JUL-2000; 2000US-0218290P.  
PR 26-JUL-2000; 2000US-0220963P.  
PR 26-JUL-2000; 2000US-0220964P.  
PR 14-AUG-2000; 2000US-0224518P.  
PR 14-AUG-2000; 2000US-0224519P.  
PR 14-AUG-2000; 2000US-0225267P.  
PR 14-AUG-2000; 2000US-0225268P.  
PR 14-AUG-2000; 2000US-0225270P.  
PR 14-AUG-2000; 2000US-0225447P.  
PR 14-AUG-2000; 2000US-0225757P.  
PR 14-AUG-2000; 2000US-0225758P.  
PR 22-AUG-2000; 2000US-0226868P.  
PR 30-AUG-2000; 2000US-0228924P.  
PR 01-SEP-2000; 2000US-0229287P.  
PR 01-SEP-2000; 2000US-0229343P.  
PR 01-SEP-2000; 2000US-0229344P.  
PR 01-SEP-2000; 2000US-0229345P.  
PR 05-SEP-2000; 2000US-0229509P.  
PR 05-SEP-2000; 2000US-0229513P.  
PR 08-SEP-2000; 2000US-0231413P.  
PR 21-SEP-2000; 2000US-0234223P.  
PR 21-SEP-2000; 2000US-0234274P.  
PR 25-SEP-2000; 2000US-0234997P.  
PR 27-SEP-2000; 2000US-0235834P.  
PR 29-SEP-2000; 2000US-0236327P.  
PR 29-SEP-2000; 2000US-0236367P.  
PR 29-SEP-2000; 2000US-0236368P.  
PR 29-SEP-2000; 2000US-0236369P.  
PR 29-SEP-2000; 2000US-0236370P.  
PR 02-OCT-2000; 2000US-0236802P.  
PR 02-OCT-2000; 2000US-0237037P.  
PR 02-OCT-2000; 2000US-0237038P.  
PR 02-OCT-2000; 2000US-0237039P.  
PR 02-OCT-2000; 2000US-0237040P.  
PR 13-OCT-2000; 2000US-0239935P.  
PR 20-OCT-2000; 2000US-0240960P.  
PR 20-OCT-2000; 2000US-0241785P.  
PR 20-OCT-2000; 2000US-0241809P.  
PR 01-NOV-2000; 2000US-0244617P.  
PR 17-NOV-2000; 2000US-0249299P.  
PR 08-DEC-2000; 2000US-0251856P.  
PR 08-DEC-2000; 2000US-0251868P.  
PR 08-DEC-2000; 2000US-0251869P.  
XX (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
XX  
XX Rosen CA, Ruben SM, Barash SC;  
XX WPI; 2003-147444/14.  
XX P-PSDB; ABUS5170.  
XX  
XX New polypeptides and nucleic acids, useful in gene therapy for treating,  
XX inhibiting or preventing e.g. neural, immune system, muscular,  
XX respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or  
XX renal disorders.  
XX  
XX Claim 1; SEQ ID NO 268; 402pp; English.  
XX  
XX The invention relates to human novel polypeptides and their associated  
XX polynucleotides. The polypeptides and polynucleotides are useful in gene  
XX therapy for treating, inhibiting or preventing neural disorders, immune  
XX system disorders (e.g. systemic lupus erythematosus, rheumatoid arthritis  
XX and multiple sclerosis), muscular disorders, respiratory diseases (e.g.  
XX nasal vestibulitis, nasal polyps and sinusitis), reproductive disorders,  
XX gastrointestinal disorders, pulmonary disorders, cardiovascular disorders  
XX (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left

CC heart syndrome), renal disorders (e.g. acute kidney failure and end-stage  
CC renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and  
CC leukemia), inflammatory diseases (e.g. septic shock, bursitis and  
CC appendicitis), allergic reactions and conditions (e.g. asthma), blood  
CC related disorders (e.g. thrombosis, atherosclerosis and myocardial  
CC infarction) and cancerous diseases. Sequences ABX73173-ABX74167 represent  
CC human novel polynucleotides of the invention  
XX  
XX Sequence 2102 BP; 538 A; 567 C; 504 G; 493 T; 0 U; 0 Other;  
SQ  
Query Match 43.5%; Score 22.2; DB 7; Length 2102;  
Best Local Similarity 77.1%; Pred. No. 46;  
Matches 27; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
QY 5 CCACCTGCTTCTTGCTTATCCGGGCAAGAACT 39  
DB 1104 CCACCGTCTTCTCTCTCTCTCCGCAAGAACT 1138  
RESULT 14  
AAH14667  
ID AAH14667 standard; cDNA; 2543 BP.  
XX  
XX AAH14667;  
XX  
XX 26-JUN-2001 (first entry)  
XX  
XX Human cDNA sequence SEQ ID NO:12347.  
DE  
XX Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.  
XX Homo sapiens.  
XX  
XX EP1074617-A2.  
XX  
XX 07-FEB-2001.  
XX  
XX 28-JUL-2000; 2000EP-00116126.  
XX  
XX 29-JUL-1999; 99JP-00248036.  
XX 27-AUG-1999; 99JP-00300253.  
XX 11-JAN-2000; 2000JP-00118776.  
XX 02-MAY-2000; 2000JP-00183767.  
XX 09-JUN-2000; 2000JP-00241899.  
XX  
XX (HELI-) HELIX RES INST.  
XX  
XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;  
XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;  
XX WPI; 2001-318749/34.  
XX  
XX Primer sets for synthesizing polynucleotides, particularly the 5602 full-  
XX length cDNAs defined in the specification, and for the detection and/or  
XX diagnosis of the abnormality of the proteins encoded by the full-length  
XX cDNAs.  
XX  
XX Claim 8; SEQ ID NO 12347; 2537pp + Sequence Listing; English.  
XX  
XX The present invention describes primer sets for synthesizing 5602 full-  
XX length cDNAs defined in the specification. Where a primer set comprises:  
XX (a) an oligo-dT primer and an oligonucleotide complementary to the  
XX complementary strand of a polynucleotide which comprises one of the 5602  
XX nucleotide sequences defined in the specification, where the  
XX oligonucleotide comprises at least 15 nucleotides; or (b) a combination  
XX of an oligonucleotide comprising a sequence complementary to the  
XX complementary strand of a polynucleotide which comprises a 5'-end  
XX sequence and an oligonucleotide comprising a sequence complementary to a  
XX polynucleotide which comprises a 3'-end sequence, where the  
XX oligonucleotide comprises at least 15 nucleotides and the combination of  
XX the 5'-end sequence/3'-end sequence is selected from those defined in the  
XX specification. The primer sets can be used in antisense therapy and in  
XX gene therapy. The primers are useful for synthesizing polynucleotides,



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OM nucleic - nucleic search, using sw model

Run on: August 2, 2004, 19:08:00 ; Search time 111.328 Seconds  
968.934 Million cell updates/sec

Title: US-10-068-067-17

Perfect score: 22

Sequence: 1 ggtaccactggtcttctgtgc 22

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 3222919 seqs, 245157024 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6445838

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA:

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- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq\*
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- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq\*
- 13: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq2\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq\*
- 17: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq\*
- 18: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq\*
- 19: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	100.0	22	14	US-10-068-067-17
2	22	100.0	51	14	Sequence 17, Appl
3	22	100.0	51	14	Sequence 16, Appl
4	22	100.0	2895	14	Sequence 21, Appl
5	21	95.5	21	14	Sequence 22, Appl
6	15	68.2	695	13	Sequence 114054,
7	15	68.2	695	13	Sequence 114055,
8	15	68.2	695	13	Sequence 114056,
9	15	68.2	695	16	Sequence 114057,
10	15	68.2	695	16	Sequence 114058,
11	15	68.2	695	16	Sequence 114059,
12	15	68.2	767	13	Sequence 14404,
13	15	68.2	767	13	Sequence 145338,
14	15	68.2	767	13	Sequence 145339,

C 15	68.2	767	13	US-10-027-632-145340	Sequence 145340, A
C 16	68.2	767	16	US-10-027-632-14404	Sequence 14404, A
C 17	68.2	767	16	US-10-027-632-145338	Sequence 145338, A
C 18	68.2	767	16	US-10-027-632-145339	Sequence 145339, A
C 19	68.2	767	16	US-10-027-632-145340	Sequence 145340, A
C 20	68.2	1251	15	US-10-198-846-13243	Sequence 13243, A
C 21	68.2	1267	13	US-10-372-876-78	Sequence 78, Appl
C 22	68.2	1267	13	US-10-097-065-78	Sequence 2831, Appl
C 23	68.2	1335	17	US-10-437-963-25606	Sequence 25606, A
C 24	68.2	1335	17	US-10-437-963-25606	Sequence 25606, A
C 25	68.2	1335	17	US-10-437-963-25606	Sequence 25606, A
C 26	68.2	2895	17	US-10-437-963-25606	Sequence 25606, A
C 27	68.2	2895	17	US-10-437-963-25606	Sequence 25606, A
C 28	68.2	3261	13	US-10-027-632-112371	Sequence 112371, A
C 29	68.2	119201	17	US-10-450-826-32	Sequence 32, Appl
C 30	68.2	118067	15	US-10-081-327-32	Sequence 232, Appl
C 31	68.2	228139	13	US-10-087-192-232	Sequence 232, Appl
C 32	68.2	25	17	US-10-717-597-2928	Sequence 2928, Appl
C 33	68.2	60	10	US-09-908-975-5528	Sequence 5528, Appl
C 34	68.2	255	17	US-10-437-963-30581	Sequence 30581, A
C 35	68.2	359	17	US-10-469-285-438	Sequence 438, Appl
C 36	68.2	390	13	US-10-424-599-11913	Sequence 11913, A
C 37	68.2	392	10	US-09-918-995-16250	Sequence 16250, A
C 38	68.2	400	10	US-09-918-995-4377	Sequence 4377, Appl
C 39	68.2	453	17	US-10-437-963-45777	Sequence 45777, A
C 40	68.2	468	9	US-09-864-761-2123	Sequence 2123, Appl
C 41	68.2	479	13	US-10-027-632-292457	Sequence 292457, A
C 42	68.2	479	16	US-10-027-632-292457	Sequence 292457, A
C 43	68.2	542	15	US-10-255-536-135	Sequence 135, Appl
C 44	68.2	545	13	US-09-770-152-602	Sequence 602, Appl
C 45	68.2	559	13	US-10-027-632-223556	Sequence 223556, A

ALIGNMENTS

RESULT 1  
US-10-068-067-17  
; Sequence 17, Application US/10068067  
; Publication No. US20020151064A1  
; GENERAL INFORMATION:  
; APPLICANT: Rothenberg, Marc E.  
; APPLICANT: Zimmermann, Nives  
; APPLICANT: Children's Hospital Medical Center  
; TITLE OF INVENTION: REGULATION OF CCR3 EXPRESSION  
; FILE REFERENCE: CMC-153  
; CURRENT APPLICATION NUMBER: US/10/068,067  
; CURRENT FILING DATE: 2002-02-05  
; PRIOR APPLICATION NUMBER: 60/267,073  
; PRIOR FILING DATE: 2001-02-07  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 17  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-068-067-17

Query Match	100.0%	Score 22;	DB 14;	Length 22;
Best Local Similarity	100.0%	Pred. No. 0.0065;		
Matches	22;	Conservative	0;	Mismatches
			0;	Indels
			0;	Gaps
			0;	
Qy	1	GGTACCACTGGTCTCTCTGTGC	22	
Db	1	GGTACCACTGGTCTCTCTGTGC	22	
RESULT 2				
US-10-068-067-16				
; Sequence 16, Application US/10068067				
; Publication No. US20020151064A1				
; GENERAL INFORMATION:				
; APPLICANT: Rothenberg, Marc E.				

```
; APPLICANT: Zimmermann, Nives
; APPLICANT: Children's Hospital Medical Center
; TITLE OF INVENTION: REGULATION OF CCR3 EXPRESSION
; FILE REFERENCE: CMC-153
; CURRENT APPLICATION NUMBER: US/10/068,067
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 60/267,073
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-068-067-16

Query Match      100.0%; Score 22; DB 14; Length 51;
Best Local Similarity 100.0%; Pred. No. 0.006;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACCACTGGTCTTCTTGTC 22
    |||||
Db 1 GGTACCACTGGTCTTCTTGTC 22

RESULT 3
US-10-068-067-21
; Sequence 21, Application US/10068067
; Publication No. US20020151064A1
; GENERAL INFORMATION:
; APPLICANT: Rothenberg, Marc E.
; APPLICANT: Zimmermann, Nives
; APPLICANT: Children's Hospital Medical Center
; TITLE OF INVENTION: REGULATION OF CCR3 EXPRESSION
; FILE REFERENCE: CMC-153
; CURRENT APPLICATION NUMBER: US/10/068,067
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 60/267,073
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 51
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-068-067-21

Query Match      100.0%; Score 22; DB 14; Length 51;
Best Local Similarity 63.6%; Pred. No. 0.006;
Matches 14; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACCACTGGTCTTCTTGTC 22
    |||||
Db 1 GGUACCACUGGUCUUCUGGC 22

RESULT 4
US-10-068-067-11
; Sequence 11, Application US/10068067
; Publication No. US20020151064A1
; GENERAL INFORMATION:
; APPLICANT: Rothenberg, Marc E.
; APPLICANT: Zimmermann, Nives
; APPLICANT: Children's Hospital Medical Center
; TITLE OF INVENTION: REGULATION OF CCR3 EXPRESSION
; FILE REFERENCE: CMC-153
; CURRENT APPLICATION NUMBER: US/10/068,067
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 60/267,073
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
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; LENGTH: 2895
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-068-067-11

Query Match      100.0%; Score 22; DB 14; Length 2895;
Best Local Similarity 100.0%; Pred. No. 0.004;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACCACTGGTCTTCTTGTC 22
    |||||
Db 1561 GGTACCACTGGTCTTCTTGTC 1582

RESULT 5
US-10-068-067-22
; Sequence 22, Application US/10068067
; Publication No. US20020151064A1
; GENERAL INFORMATION:
; APPLICANT: Rothenberg, Marc E.
; APPLICANT: Zimmermann, Nives
; APPLICANT: Children's Hospital Medical Center
; TITLE OF INVENTION: REGULATION OF CCR3 EXPRESSION
; FILE REFERENCE: CMC-153
; CURRENT APPLICATION NUMBER: US/10/068,067
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 60/267,073
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-068-067-22

Query Match      95.58%; Score 21; DB 14; Length 21;
Best Local Similarity 61.9%; Pred. No. 0.024;
Matches 13; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACCACTGGTCTTCTTGTC 21
    |||||
Db 1 GGUACCACUGGUCUUCUGGC 21

RESULT 6
US-10-027-632-114054
; Sequence 114054, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 114054
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```
; LENGTH: 695
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-114054

Query Match          68.2%; Score 15; DB 13; Length 695;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ACTGGTCTTCTTG 21
Db 464 ACTGGTCTTCTTG 478

RESULT 7
US-10-027-632-114055
; Sequence 114055, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 114055
; LENGTH: 695
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-114055

Query Match          68.2%; Score 15; DB 13; Length 695;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ACTGGTCTTCTTG 21
Db 464 ACTGGTCTTCTTG 478

RESULT 8
US-10-027-632-114056
; Sequence 114056, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 114056
; LENGTH: 695
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-114056

Query Match          68.2%; Score 15; DB 13; Length 695;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ACTGGTCTTCTTG 21
Db 464 ACTGGTCTTCTTG 478
```

```
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 114054
; LENGTH: 695
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-114054

Query Match          68.2%; Score 15; DB 13; Length 695;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ACTGGTCTTCTTG 21
Db 464 ACTGGTCTTCTTG 478

RESULT 9
US-10-027-632-114054
; Sequence 114054, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 114054
; LENGTH: 695
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-114054

Query Match          68.2%; Score 15; DB 16; Length 695;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ACTGGTCTTCTTG 21
Db 464 ACTGGTCTTCTTG 478

RESULT 10
US-10-027-632-114055
; Sequence 114055, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
```

;; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
;; FILE REFERENCE: 108827.129  
;; CURRENT APPLICATION NUMBER: US/10/027,632  
;; CURRENT FILING DATE: 2002-04-30

;; PRIOR APPLICATION NUMBER: US 60/218,006  
;; PRIOR FILING DATE: 2000-07-12  
;; PRIOR APPLICATION NUMBER: US 60/198,676  
;; PRIOR FILING DATE: 2000-04-20  
;; PRIOR APPLICATION NUMBER: US 60/193,483  
;; PRIOR FILING DATE: 2000-03-29  
;; PRIOR APPLICATION NUMBER: US 60/185,218  
;; PRIOR FILING DATE: 2000-02-24  
;; PRIOR APPLICATION NUMBER: US 60/167,363  
;; PRIOR FILING DATE: 1999-11-23  
;; PRIOR APPLICATION NUMBER: US 60/156,358  
;; PRIOR FILING DATE: 1999-09-28  
;; PRIOR APPLICATION NUMBER: US 60/146,002  
;; PRIOR FILING DATE: 1999-08-09  
;; NUMBER OF SEQ ID NOS: 325720  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 114055  
;; LENGTH: 695  
;; TYPE: DNA  
;; ORGANISM: Human  
US-10-027-632-114055

Query Match 68.2%; Score 15; DB 15; Length 695;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ACTGGTCTTCTTG 21  
Db 464 ACTGGTCTTCTTG 478

## RESULT 11

US-10-027-632-114056  
;; Sequence 114056, Application US/10027632  
;; Publication No. US20030204075A9  
;; GENERAL INFORMATION:  
;; APPLICANT: Wang, David G.  
;; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
;; FILE REFERENCE: 108827.129  
;; CURRENT APPLICATION NUMBER: US/10/027,632  
;; CURRENT FILING DATE: 2002-04-30  
;; PRIOR APPLICATION NUMBER: US 60/218,006  
;; PRIOR FILING DATE: 2000-07-12  
;; PRIOR APPLICATION NUMBER: US 60/198,676  
;; PRIOR FILING DATE: 2000-04-20  
;; PRIOR APPLICATION NUMBER: US 60/193,483  
;; PRIOR FILING DATE: 2000-03-29  
;; PRIOR APPLICATION NUMBER: US 60/185,218  
;; PRIOR FILING DATE: 2000-02-24  
;; PRIOR APPLICATION NUMBER: US 60/167,363  
;; PRIOR FILING DATE: 1999-11-23  
;; PRIOR APPLICATION NUMBER: US 60/156,358  
;; PRIOR FILING DATE: 1999-09-28  
;; PRIOR APPLICATION NUMBER: US 60/146,002  
;; PRIOR FILING DATE: 1999-08-09  
;; NUMBER OF SEQ ID NOS: 325720  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 114056  
;; LENGTH: 695  
;; TYPE: DNA  
;; ORGANISM: Human  
US-10-027-632-114056

Query Match 68.2%; Score 15; DB 16; Length 695;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ACTGGTCTTCTTG 21  
Db 464 ACTGGTCTTCTTG 478

## RESULT 12

US-10-027-632-14404/c  
;; Sequence 14404, Application US/10027632  
;; Publication No. US20020198371A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Wang, David G.  
;; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
;; FILE REFERENCE: 108827.129  
;; CURRENT APPLICATION NUMBER: US/10/027,632  
;; CURRENT FILING DATE: 2002-04-30  
;; PRIOR APPLICATION NUMBER: US 60/218,006  
;; PRIOR FILING DATE: 2000-07-12  
;; PRIOR APPLICATION NUMBER: US 60/198,676  
;; PRIOR FILING DATE: 2000-04-20  
;; PRIOR APPLICATION NUMBER: US 60/193,483  
;; PRIOR FILING DATE: 2000-03-29  
;; PRIOR APPLICATION NUMBER: US 60/185,218  
;; PRIOR FILING DATE: 2000-02-24  
;; PRIOR APPLICATION NUMBER: US 60/167,363  
;; PRIOR FILING DATE: 1999-11-23  
;; PRIOR APPLICATION NUMBER: US 60/156,358  
;; PRIOR FILING DATE: 1999-09-28  
;; PRIOR APPLICATION NUMBER: US 60/146,002  
;; PRIOR FILING DATE: 1999-08-09  
;; NUMBER OF SEQ ID NOS: 325720  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 14404  
;; LENGTH: 767  
;; TYPE: DNA  
;; ORGANISM: Human  
US-10-027-632-14404

Query Match 68.2%; Score 15; DB 13; Length 767;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ACCACTGCTCTTCTT 18  
Db 628 ACCACTGCTCTTCTT 614

## RESULT 13

US-10-027-632-145338/c  
;; Sequence 145338, Application US/10027632  
;; Publication No. US20020198371A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Wang, David G.  
;; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
;; FILE REFERENCE: 108827.129  
;; CURRENT APPLICATION NUMBER: US/10/027,632  
;; CURRENT FILING DATE: 2002-04-30  
;; PRIOR APPLICATION NUMBER: US 60/218,006  
;; PRIOR FILING DATE: 2000-07-12  
;; PRIOR APPLICATION NUMBER: US 60/198,676  
;; PRIOR FILING DATE: 2000-04-20  
;; PRIOR APPLICATION NUMBER: US 60/193,483  
;; PRIOR FILING DATE: 2000-03-29  
;; PRIOR APPLICATION NUMBER: US 60/185,218  
;; PRIOR FILING DATE: 2000-02-24  
;; PRIOR APPLICATION NUMBER: US 60/167,363  
;; PRIOR FILING DATE: 1999-11-23  
;; PRIOR APPLICATION NUMBER: US 60/156,358  
;; PRIOR FILING DATE: 1999-09-28  
;; PRIOR APPLICATION NUMBER: US 60/146,002  
;; PRIOR FILING DATE: 1999-08-09  
;; NUMBER OF SEQ ID NOS: 325720



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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 145338
; LENGTH: 767
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-145338
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```
Query Match      68.2%; Score 15; DB 13; Length 767;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4  ACCACTGGTCTTCTT 18
      |||||
Db      628  ACCACTGGTCTTCTT 614
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## RESULT 14

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US-10-027-632-145339/c
; Sequence 145339, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
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```
; APPLICANT: Wang, David G.
```

```
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
```

```
; FILE OF INVENTION: Polymorphisms in the Human Genome
```

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; FILE REFERENCE: 108827.129
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; CURRENT APPLICATION NUMBER: US/10/027,632
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; CURRENT FILING DATE: 2002-04-30
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; PRIOR APPLICATION NUMBER: US 60/218,006
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; PRIOR FILING DATE: 2000-07-12
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; PRIOR APPLICATION NUMBER: US 60/198,676
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; PRIOR FILING DATE: 2000-04-20
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; PRIOR APPLICATION NUMBER: US 60/193,483
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; PRIOR FILING DATE: 2000-03-29
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; PRIOR APPLICATION NUMBER: US 60/185,218
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; PRIOR FILING DATE: 2000-02-24
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; PRIOR APPLICATION NUMBER: US 60/167,363
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; PRIOR FILING DATE: 1999-11-23
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; PRIOR APPLICATION NUMBER: US 60/156,358
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; PRIOR FILING DATE: 1999-09-28
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; PRIOR APPLICATION NUMBER: US 60/146,002
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; PRIOR FILING DATE: 1999-08-09
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; NUMBER OF SEQ ID NOS: 325720
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```
; SOFTWARE: FastSEQ for Windows Version 4.0
```

```
; SEQ ID NO 145339
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; LENGTH: 767
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; TYPE: DNA
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```
; ORGANISM: Human
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US-10-027-632-145339
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Query Match      68.2%; Score 15; DB 13; Length 767;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      4  ACCACTGGTCTTCTT 18
      |||||
Db      628  ACCACTGGTCTTCTT 614
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## RESULT 15

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US-10-027-632-145340/c
; Sequence 145340, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
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; APPLICANT: Wang, David G.
```

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; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
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; FILE OF INVENTION: Polymorphisms in the Human Genome
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; FILE REFERENCE: 108827.129
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; CURRENT APPLICATION NUMBER: US/10/027,632
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; CURRENT FILING DATE: 2002-04-30
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; PRIOR APPLICATION NUMBER: US 60/218,006
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; PRIOR FILING DATE: 2000-07-12
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; PRIOR APPLICATION NUMBER: US 60/198,676
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; PRIOR FILING DATE: 2000-04-20
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; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 145340
; LENGTH: 767
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-145340
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Query Match      68.2%; Score 15; DB 13; Length 767;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      4  ACCACTGGTCTTCTT 18
      |||||
Db      628  ACCACTGGTCTTCTT 614
```

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Job time : 112.328 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 2, 2004, 16:56:38 ; Search time 106.207 Seconds

(without alignments)  
879.984 Million cell updates/sec

Title: US-10-068-067-17

Perfect score: 22  
Sequence: 1 ggtaccactgggtcttcttgc 22

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 337863 seqs, 212409041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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- 1: geneseq1980s.\*
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- 6: geneseq2002s.\*
- 7: geneseq2003as.\*
- 8: geneseq2003bs.\*
- 9: geneseq2003cs.\*
- 10: geneseq2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	100.0	22	6	ABQ78515 Nucleotid
2	22	100.0	51	6	ABQ78514 Nucleotid
3	22	100.0	51	6	ABQ78519 Nucleotid
4	22	100.0	2895	6	ABQ78513 Nucleotid
5	21	95.5	21	6	ABQ78520 Nucleotid
6	16	72.7	406	9	ADb51450 Primary r
7	15	68.2	240	3	AAa61159 SEN virus
8	15	68.2	249	6	ABn16387 Human ORF
9	15	68.2	278	3	AAa61168 SEN virus
10	15	68.2	700	4	AAh92754 Human inf
11	15	68.2	700	4	AAh92753 Human inf
12	15	68.2	823	5	ABv10808 Human pro
13	15	68.2	1076	3	AAC45720 Arabidops
14	15	68.2	1078	3	AAC41924 Arabidops
15	15	68.2	1267	2	AAx97978 Human sec
16	15	68.2	1267	8	ADa11550 Human cDN
17	15	68.2	2000	7	ADa72241 Rice gene
18	15	68.2	5046	4	AAa01709 Chicken c
19	15	68.2	5450	6	ACf05021 Human cat
20	15	68.2	109201	8	ABq88125 Human ost
21	14	63.6	22	4	AAa14515 Human GST
22	14	63.6	31	6	ABa04121 Human CSP
23	14	63.6	60	6	ABn32780 Human spl

24	14	63.6	359	4	AAK53873	Murine re
25	14	63.6	378	5	AAf64835	Novel hum
26	14	63.6	392	8	ACH29038	Human adu
27	14	63.6	400	8	ACH17165	Human adu
28	14	63.6	468	4	AAI12202	Probe #21
29	14	63.6	468	4	ABA53909	Human foe
30	14	63.6	468	4	AAI33552	Probe #22
31	14	63.6	468	4	AAI33552	Human bre
32	14	63.6	468	4	ABA43455	Human bre
33	14	63.6	468	4	AAK23657	Probe #21
34	14	63.6	468	4	AAK27622	Human bon
35	14	63.6	468	4	AAK02175	Human bra
36	14	63.6	468	4	ABs27192	Human liv
37	14	63.6	468	5	AAI02114	Probe #21
38	14	63.6	468	6	ABs02085	Human gen
39	14	63.6	521	4	AAK89500	Human dig
40	14	63.6	537	4	ABv48958	Human pro
41	14	63.6	540	5	AAa05535	Mammalian
42	14	63.6	545	7	ABX57250	Arabidops
43	14	63.6	568	3	AAc34694	Arabidops
44	14	63.6	600	4	AAa11098	Human cal
45	14	63.6	601	3	AAf11306	Aspergill

#### ALIGNMENTS

#### RESULT 1

ABQ78515  
ID ABQ78515 standard; DNA; 22 BP.  
XX AC ABQ78515;  
XX DT 25-NOV-2002 (first entry)  
XX DE Nucleotide sequence of a regulatory sequence for human CCR3.  
XX Human; CC chemokine receptor 3; CCR3; allergic disorder; probe;  
KW inflammatory disorder; eosinophil; hypersensitivity; leukemia;  
KW infectious disorder; HIV; respiratory syncytial virus infection; ss.  
XX OS Homo sapiens.  
XX PN WO200262848-A2.  
XX PD 15-AUG-2002.  
XX PF 06-FEB-2002; 2002WO-US003442.  
XX PR 07-FEB-2001; 2001US-0267073P.  
XX PR 05-FEB-2002; 2002US-00068067.  
(CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
(Rothenberg WE, Zimmerman N;  
WPI; 2002-657524/70.  
New CC chemokine receptor 3 (CCR3) regulatory site in an untranslated  
exon 1, exon 2, exon 3 or promoter of a human CCR3 gene or mRNA capable  
of binding to regulatory elements, useful for preventing e.g. allergic  
inflammatory reactions.  
Claim 6; Page 54; 56pp; English.  
The present sequence represents a probe for the human CC chemokine  
receptor 3 (CCR3) gene. The probe is a regulatory sequence for CCR3. CCR3  
is expressed on cells involved in allergic and/or inflammatory disorders.  
The gene comprises 4 exons, with the coding region present on exon 4. The  
specification describes methods of regulating the expression of CCR3. The  
regulatory site is derived from an untranslated exon 1, exon 2, exon 3 or  
promoter of a human CCR3 gene. Regulating the expression of the chemokine  
receptor CCR3 is useful for preventing or treating disorders involving

CC eosinophils, such as allergic inflammatory and hypersensitivity  
 CC reactions, certain types of leukemia, and certain infectious disorders  
 CC involving CCR3, e.g. HIV or respiratory syncytial virus infection.  
 CC Expression and modulation of CCR3 is a useful tool in assessing  
 CC eosinophil targeting and in regulating eosinophil-mediated reactions and  
 CC diseases  
 XX  
 SQ Sequence 22 BP; 2 A; 6 C; 6 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 6; Length 22;  
 Best Local Similarity 100.0%; Pred. NO. 0.017;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACCACTGGTCTCTTGTC 22  
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 DB 1 GGTACCACTGGTCTCTTGTC 22

RESULT 2  
 ABQ78514  
 ID ABQ78514 standard; DNA; 51 BP.  
 XX  
 AC ABQ78514;  
 XX  
 DT 25-NOV-2002 (first entry)  
 XX  
 DE Nucleotide sequence of a regulatory sequence for human CCR3.  
 XX  
 KW Human; CC chemokine receptor 3; CCR3; allergic disorder; probe;  
 KW inflammatory disorder; eosinophil; hypersensitivity; leukemia;  
 KW infectious disorder; HIV; respiratory syncytial virus infection; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT misc\_binding 24..27  
 FT /\*tag= a  
 FT /note= "transcription factor binding site for GATA"  
 FT misc\_binding 40..43  
 FT /\*tag= b  
 FT /note= "transcription factor binding site for GATA"  
 XX  
 PN WO200262848-A2.  
 XX  
 PD 15-AUG-2002.  
 XX  
 PF 06-FEB-2002; 2002WO-US003442.  
 XX  
 PR 07-FEB-2001; 2001US-0267073P.  
 XX  
 PR 05-FEB-2002; 2002US-00068067.  
 XX  
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
 XX  
 PI Rothenberg ME, Zimmerman N;  
 XX  
 WPI; 2002-657524/70.  
 XX  
 DR New CC chemokine receptor 3 (CCR3) regulatory site in an untranslated  
 PT exon 1, exon 2, exon 3 or promoter of a human CCR3 gene or mRNA capable  
 PT of binding to regulatory elements, useful for preventing e.g. allergic  
 PT inflammatory reactions.  
 XX  
 PS Claim 2; Page 25; 56pp; English.  
 XX  
 CC The present sequence represents a probe for the human CC chemokine  
 CC receptor 3 (CCR3) gene. The probe comprises +10 to +60 of exon 1 of CCR3,  
 CC and is a regulatory sequence for CCR3. CCR3 is expressed on cells  
 CC involved in allergic and/or inflammatory disorders. The gene comprises 4  
 CC exons, with the coding region present on exon 4. The specification  
 CC describes methods of regulating the expression of CCR3. The regulatory  
 CC site is derived from an untranslated exon 1, exon 2, exon 3 or promoter  
 CC of a human CCR3 gene. Regulating the expression of the chemokine receptor  
 CC CCR3 is useful for preventing or treating disorders involving

CC eosinophils, such as allergic inflammatory and hypersensitivity  
 CC reactions, certain types of leukemia, and certain infectious disorders  
 CC involving CCR3, e.g. HIV or respiratory syncytial virus infection.  
 CC Expression and modulation of CCR3 is a useful tool in assessing  
 CC eosinophil targeting and in regulating eosinophil-mediated reactions and  
 CC diseases  
 XX  
 SQ Sequence 51 BP; 13 A; 12 C; 11 G; 15 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 6; Length 51;  
 Best Local Similarity 100.0%; Pred. NO. 0.017;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACCACTGGTCTCTTGTC 22  
 |||||  
 DB 1 GGTACCACTGGTCTCTTGTC 22

RESULT 3  
 ABQ78519  
 ID ABQ78519 standard; RNA; 51 BP.  
 XX  
 AC ABQ78519;  
 XX  
 DT 25-NOV-2002 (first entry)  
 XX  
 DE Nucleotide sequence of a regulatory sequence for human CCR3.  
 XX  
 KW Human; CC chemokine receptor 3; CCR3; allergic disorder; probe;  
 KW inflammatory disorder; eosinophil; hypersensitivity; leukemia;  
 KW infectious disorder; HIV; respiratory syncytial virus infection; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200262848-A2.  
 XX  
 PD 15-AUG-2002.  
 XX  
 PF 06-FEB-2002; 2002WO-US003442.  
 XX  
 PR 07-FEB-2001; 2001US-0267073P.  
 XX  
 PR 05-FEB-2002; 2002US-00068067.  
 XX  
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
 XX  
 PI Rothenberg ME, Zimmerman N;  
 XX  
 WPI; 2002-657524/70.  
 XX  
 DR New CC chemokine receptor 3 (CCR3) regulatory site in an untranslated  
 PT exon 1, exon 2, exon 3 or promoter of a human CCR3 gene or mRNA capable  
 PT of binding to regulatory elements, useful for preventing e.g. allergic  
 PT inflammatory reactions.  
 XX  
 PS Claim 7; Page 56; 56pp; English.  
 XX  
 CC The present sequence represents a probe for the human CC chemokine  
 CC receptor 3 (CCR3) gene. The probe is a regulatory sequence for CCR3. CCR3  
 CC is expressed on cells involved in allergic and/or inflammatory disorders.  
 CC The gene comprises 4 exons, with the coding region present on exon 4. The  
 CC specification describes methods of regulating the expression of CCR3. The  
 CC regulatory site is derived from an untranslated exon 1, exon 2, exon 3 or  
 CC promoter of a human CCR3 gene. Regulating the expression of the chemokine  
 CC receptor CCR3 is useful for preventing or treating disorders involving  
 CC eosinophils, such as allergic inflammatory and hypersensitivity  
 CC reactions, certain types of leukemia, and certain infectious disorders  
 CC involving CCR3, e.g. HIV or respiratory syncytial virus infection.  
 CC Expression and modulation of CCR3 is a useful tool in assessing  
 CC eosinophil targeting and in regulating eosinophil-mediated reactions and  
 CC diseases  
 XX  
 SQ Sequence 51 BP; 13 A; 12 C; 11 G; 0 T; 15 U; 0 Other;

Query Match 100.0%; Score 22; DB 6; Length 51;  
 Best Local Similarity 63.6%; Pred. No. 0.017; 0; Indels 0; Gaps 0;  
 Matches 14; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTACCACTGGTCTCTTGTGC 22  
 Db 1 GGUACCACUGGUCUUCUUGGC 22

RESULT 4  
 ABO78513  
 ID ABO78513 standard; DNA; 2895 BP.

XX AC ABO78513;  
 XX DT 25-NOV-2002 (first entry)  
 XX DE Nucleotide sequence of the human CCR3 gene promoter.  
 XX KW Human; CC chemokine receptor 3; CCR3; allergic disorder;  
 XX KW inflammatory disorder; eosinophil; hypersensitivity; leukemia;  
 XX KW infectious disorder; HIV; respiratory syncytial virus infection;  
 XX KW promoter; ss.

XX OS Homo sapiens.  
 XX PF Key Location/Qualifiers  
 XX PH misc\_signal 1640..1645  
 XX FT /\*tag= a  
 XX FT /note= "splice donor consensus site"

XX FN WO200262848-A2.  
 XX PD 15-AUG-2002.  
 XX PF 06-FEB-2002; 2002WO-US003442.  
 XX PR 07-FEB-2001; 2001US-0267073P.  
 XX PR 05-FEB-2002; 2002US-00068067.

XX PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
 XX PI Rothenberg ME, Zimmerman N;  
 XX DR WPI; 2002-657524/70.

XX PT New CC chemokine receptor 3 (CCR3) regulatory site in an untranslated  
 XX PT exon 1, exon 2, exon 3 or promoter of a human CCR3 gene or mRNA capable  
 XX PT of binding to regulatory elements, useful for preventing e.g. allergic  
 XX PT inflammatory reactions.

XX PS Disclosure; Fig 4; 56pp; English.  
 XX CC The present sequence represents the promoter of the human CC chemokine  
 XX CC receptor 3 (CCR3) gene. CCR3 is expressed on cells involved in allergic  
 XX CC and/or inflammatory disorders. The gene comprises 4 exons, with the  
 XX CC coding region present on exon 4. The specification describes methods of  
 XX CC regulating the expression of CCR3. The regulatory site is derived from an  
 XX CC untranslated exon 1, exon 2, exon 3 or promoter of a human CCR3 gene.  
 XX CC Regulating the expression of the chemokine receptor CCR3 is useful for  
 XX CC preventing or treating disorders involving eosinophils, such as allergic  
 XX CC inflammatory and hypersensitivity reactions, certain types of leukemia,  
 XX CC and certain infectious disorders involving CCR3, e.g. HIV or respiratory  
 XX CC syncytial virus infection. Expression and modulation of CCR3 is a useful  
 XX CC tool in assessing eosinophil targeting and in regulating eosinophil-  
 XX CC mediated reactions and diseases

XX SQ Sequence 2895 BP; 829 A; 590 C; 556 G; 920 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 6; Length 2895;  
 Best Local Similarity 100.0%; Pred. No. 0.016; 0; Indels 0; Gaps 0;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTACCACTGGTCTCTTGTGC 22  
 Db 1561 GGTACCACTGGTCTCTTGTGC 1582

RESULT 5  
 ABO78520  
 ID ABO78520 standard; RNA; 21 BP.

XX AC ABO78520;  
 XX DT 25-NOV-2002 (first entry)  
 XX DE Nucleotide sequence of a regulatory sequence for human CCR3.

XX KW Human; CC chemokine receptor 3; CCR3; allergic disorder; probe;  
 XX KW inflammatory disorder; eosinophil; hypersensitivity; leukemia;  
 XX KW infectious disorder; HIV; respiratory syncytial virus infection; ss.

XX OS Homo sapiens.  
 XX FN WO200262848-A2.  
 XX PD 15-AUG-2002.

XX PF 06-FEB-2002; 2002WO-US003442.  
 XX PR 07-FEB-2001; 2001US-0267073P.  
 XX PR 05-FEB-2002; 2002US-00068067.

XX PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
 XX PI Rothenberg ME, Zimmerman N;  
 XX DR WPI; 2002-657524/70.

XX PT New CC chemokine receptor 3 (CCR3) regulatory site in an untranslated  
 XX PT exon 1, exon 2, exon 3 or promoter of a human CCR3 gene or mRNA capable  
 XX PT of binding to regulatory elements, useful for preventing e.g. allergic  
 XX PT inflammatory reactions.

XX PS Claim 8; Page 56; 56pp; English.

XX CC The present sequence represents a probe for the human CC chemokine  
 XX CC receptor 3 (CCR3) gene. The probe is a regulatory sequence for CCR3. CCR3  
 XX CC is expressed on cells involved in allergic and/or inflammatory disorders.  
 XX CC The gene comprises 4 exons, with the coding region present on exon 4. The  
 XX CC specification describes methods of regulating the expression of CCR3. The  
 XX CC regulatory site is derived from an untranslated exon 1, exon 2, exon 3 or  
 XX CC promoter of a human CCR3 gene. Regulating the expression of the chemokine  
 XX CC receptor CCR3 is useful for preventing or treating disorders involving  
 XX CC eosinophils, such as allergic inflammatory and hypersensitivity  
 XX CC reactions, certain types of leukemia, and certain infectious disorders  
 XX CC involving CCR3, e.g. HIV or respiratory syncytial virus infection.  
 XX CC Expression and modulation of CCR3 is a useful tool in assessing  
 XX CC eosinophil targeting and in regulating eosinophil-mediated reactions and  
 XX CC diseases

XX SQ Sequence 21 BP; 2 A; 5 C; 6 G; 0 T; 8 U; 0 Other;

Query Match 95.5%; Score 21; DB 6; Length 21;  
 Best Local Similarity 61.9%; Pred. No. 0.06;  
 Matches 13; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTACCACTGGTCTCTTGTGC 21  
 Db 1 GGUACCACUGGUCUUCUUGUG 21

RESULT 6  
 ADB51450/c  
 ID ADB51450 standard; DNA; 406 BP.  
 XX

AC ADB51450;  
 XX  
 DT 04-DEC-2003 (first entry)  
 XX  
 DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:1992.  
 XX  
 KW toxic effect; gene expression profile; hepatotoxicity; diagnostic marker;  
 KW toxicity marker; toxicity progression; drug screening;  
 KW primary rat hepatocyte toxicity modelling; gene; ds.  
 XX  
 OS Rattus norvegicus.  
 XX  
 EN WO2003065993-A2.  
 XX  
 PD 14-AUG-2003.  
 XX  
 PF 04-FEB-2003; 2003WO-US003482.  
 XX  
 PR 04-FEB-2002; 2002US-0353171P.  
 PR 13-MAR-2002; 2002US-0363534P.  
 PR 08-APR-2002; 2002US-0370248P.  
 PR 10-APR-2002; 2002US-0371134P.  
 PR 10-APR-2002; 2002US-0371135P.  
 PR 10-APR-2002; 2002US-0371150P.  
 PR 11-APR-2002; 2002US-0371413P.  
 PR 13-APR-2002; 2002US-0373601P.  
 PR 19-APR-2002; 2002US-0373602P.  
 PR 22-APR-2002; 2002US-0374139P.  
 PR 08-MAY-2002; 2002US-0378373P.  
 PR 09-MAY-2002; 2002US-0378652P.  
 PR 09-MAY-2002; 2002US-0378653P.  
 PR 09-MAY-2002; 2002US-0378655P.  
 PR 09-JUL-2002; 2002US-0394230P.  
 PR 09-JUL-2002; 2002US-0394253P.  
 PR 04-SEP-2002; 2002US-0407688P.  
 PR 28-JAN-2003; 2003US-0442900P.  
 XX  
 PA (GENE-) GENE LOGIC INC.  
 XX  
 PI Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Orr M;  
 PI Elashoff M;  
 XX  
 XX WPI; 2003-731472/69.  
 XX  
 PT Determining if a compound induces a toxic effect on a tissue or cell, for  
 PT identifying hepatotoxic compounds, comprises comparing a gene expression  
 PT profile of a tissue or cell sample to a database of Tox mean and non-Tox  
 PT mean values.  
 XX  
 XX Claim 44; SEQ ID NO 1992; 874pp; English.  
 PS  
 XX The present invention describes a method for determining whether a  
 CC compound induces a toxic effect on a tissue or cell. The method comprises  
 CC preparing a gene expression profile of a tissue or cell sample exposed to  
 CC the compound, and comparing the gene expression profile to a database  
 CC comprising data or information on the Tox mean and non-Tox mean value.  
 CC The method is useful for predicting or identifying at least one toxic  
 CC effect, particularly hepatotoxicity, of a test or unknown compound. The  
 CC genes listed in the specification are useful as diagnostic or toxicity  
 CC markers for the prediction or identification of the physiological state  
 CC of tissue or cell sample that has been exposed to a compound, or to  
 CC identify or predict the toxic effects of a compound or an agent. These  
 CC may also be used as markers for monitoring toxicity progression or for  
 CC drug screening. The present sequence represents a primary rat hepatocyte  
 CC toxicity modelling related gene sequence from the present invention.  
 XX  
 XX Sequence 406 BP; 130 A; 95 C; 87 G; 94 T; 0 U; 0 Other;  
 SQ  
 Query Match 72.7%; Score 16; DB 9; Length 406;  
 Best Local Similarity 100.0%; Pred. No. 28;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 6 CACTGGTCTTCTGTG 21

DB 129 CACTGGTCTTCTGTG 114  
 RESULT 7  
 AAA61159/c  
 ID AAA61159 standard; DNA; 240 BP.  
 XX  
 AC AAA61159;  
 XX  
 DT 12-OCT-2000 (first entry)  
 XX  
 DE SEN virus genome fragment SEQ ID NO: 116.  
 XX  
 KW SEN virus; SENV; gastrointestinal tract disorder; inflammatory disease;  
 KW proliferative disorder; hepatopathy; hepatitis; viral infection;  
 KW vaccination; gene therapy; ds.  
 XX  
 OS Hepatitis virus.  
 XX  
 PN WO200028039-A2.  
 XX  
 PD 18-MAY-2000.  
 XX  
 PF 09-NOV-1999; 99WO-EP008566.  
 XX  
 PR 10-NOV-1998; 98IT-MI002437.  
 PR 30-APR-1999; 99IT-MI000923.  
 PR 14-MAY-1999; 99EP-00830298.  
 PR 16-JUL-1999; 99EP-00113932.  
 XX  
 PA (DIAS-) DIASORIN SRL.  
 XX  
 PI Primi D, Fiordalisi G, Mantero GL, Mattioli S, Sottini A;  
 PI Bonelli F, Vaglini L, Olivero P, Dal Corso A, Bonelli M;  
 XX  
 XX WPI; 2000-376551/32.  
 XX  
 PT Nucleic acids representing the genome of the SEN virus (SENV) and encoded  
 PT proteins, useful for treatment of hepatopathies, inflammatory diseases  
 PT and proliferative disorders such as cancer.  
 XX  
 PS Claim 1; Page 353; 392pp; English.  
 XX  
 CC The present invention is concerned with the sequence of the genome of the  
 CC SEN virus (SENV), and the proteins encoded by it. SENV is thought to be  
 CC the cause of hepatopathies which are not linked to the presence of the  
 CC hepatitis A, B and E viruses in man. The genome and proteins of this  
 CC virus can be used in gene therapy and vaccination against the virus,  
 CC which also causes disorders of the gastrointestinal tract, including  
 CC Crohn's disease and lupus erythematosus, inflammatory diseases, and  
 CC proliferative disorders such as cancer  
 XX  
 XX Sequence 240 BP; 70 A; 57 C; 46 G; 67 T; 0 U; 0 Other;  
 SQ  
 Query Match 68.2%; Score 15; DB 3; Length 240;  
 Best Local Similarity 100.0%; Pred. No. 99;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 2 GTACCACTGGTCTTC 16  
 DB 28 GTACCACTGGTCTTC 14  
 RESULT 8  
 AEN16387/c  
 ID AEN16387 standard; cDNA; 249 BP.  
 XX  
 AC AEN16387;  
 XX  
 DT 24-JUN-2002 (first entry)  
 XX  
 DE Human ORFX polynucleotide sequence SEQ ID NO:1251.

XX Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;  
 KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;  
 KW degenerative disorder; osteoarthritis; neurodegenerative disorder;  
 KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;  
 KW hypertension; hypothyroidism; cholesterol ester storage disease;  
 KW immune deficiency; immune disorder; infectious disease;  
 KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;  
 KW myasthenia gravis; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200192523-A2.  
 XX  
 PD 06-DEC-2001.  
 XX  
 PF 29-MAY-2001; 2001WO-US0108936.  
 XX  
 PR 30-MAY-2000; 2000US-0206132P.  
 PR 29-AUG-2000; 2000US-0228716P.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 XX  
 PI Shinkets RA, Leach MD;  
 XX  
 DR WPI; 2002-106308/14.  
 DR P-PSDB; ABP00635.  
 XX  
 PT Novel human polypeptides and polynucleotides useful for diagnosing,  
 PT preventing and treating cardiovascular disease, neurodegenerative,  
 PT hyperproliferative disorders and autoimmune disorders.  
 XX  
 PS Disclosure; SEQ ID NO 1251; 1037pp; English.  
 XX  
 CC The present invention describes substantially purified human proteins  
 CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1  
 CC in the specification). ABN5762 to ASN27252 encode the human ORFX  
 CC proteins given in ABP0010 to ABP11500. ORFX proteins are useful for  
 CC treating or preventing a pathology associated with an ORFX-associated  
 CC disorder in humans, and in the manufacture of a medicament for treating a  
 CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide  
 CC sequences can be used in gene therapy. ORFX sequences can be used in the  
 CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,  
 CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,  
 CC osteoarthritis, neurodegenerative disorders, disorders related to organ  
 CC transplantation, cardiovascular diseases, diabetes mellitus, systemic  
 CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester  
 CC storage disease, various immune deficiencies and disorders, infectious  
 CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid  
 CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host  
 CC disease and autoimmune inflammatory eye disease. ORFX proteins are also  
 CC useful for treating burns, incisions, ulcers, for treating osteoporosis,  
 CC bone degenerative disorders, or periodontal disease, and for gut  
 CC protection or regeneration and treatment of lung or liver fibrosis,  
 CC reperfusion injury in various tissues and conditions resulting from  
 CC systemic cytokine damage. N.B. The sequence data for this patent did not  
 CC form part of the printed specification, but was obtained in electronic  
 CC format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 249 BP; 60 A; 58 C; 74 G; 57 T; 0 U; 0 Other;  
 Query Match 68.2%; Score 15; DB 6; Length 249;  
 Best Local Similarity 100.0%; Pred. No. 99;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 TACCACCTGGTCTCT 17  
 DB 38 TACCACCTGGTCTCT 24  
 RESULT 9  
 AAA61168/c  
 ID AAA61168 standard; DNA; 278 BP.

XX AAA61168;  
 AC 12-OCT-2000 (first entry)  
 DT  
 DE SEN virus genome fragment SEQ ID NO: 177.  
 DE  
 KW SEN virus; SENV; gastrointestinal tract disorder; inflammatory disease;  
 KW proliferative disorder; hepatopathy; hepatitis; viral infection;  
 KW vaccination; gene therapy; ds.  
 KW  
 XX Hepatitis virus.  
 OS  
 XX  
 PN WO2000028039-A2.  
 XX  
 PD 18-MAY-2000.  
 XX  
 PF 09-NOV-1999; 99WO-EP008566.  
 XX  
 PR 10-NOV-1998; 98IT-MI002437.  
 PR 30-APR-1999; 99IT-MI000923.  
 PR 14-MAY-1999; 99EP-00830298.  
 PR 16-JUL-1999; 99EP-00113932.  
 XX  
 PA (DIAS-) DIASORIN SRL.  
 XX  
 PI Primi D, Fiordalisi G, Mantero GL, Mattioli S, Sottini A;  
 PI Bonelli F, Vaglini L, Olivero P, Dal Corso A, Bonelli M;  
 XX  
 DR WPI; 2000-376551/32.  
 XX  
 PT Nucleic acids representing the genome of the SEN virus (SENV) and encoded  
 PT proteins, useful for treatment of hepatopathies, inflammatory diseases  
 PT and proliferative disorders such as cancer.  
 XX  
 PS Claim 1; Page 371; 392pp; English.  
 XX  
 CC The present invention is concerned with the sequence of the genome of the  
 CC SEN virus (SENV), and the proteins encoded by it. SENV is thought to be  
 CC the cause of hepatopathies which are not linked to the presence of the  
 CC hepatitis A, B and E viruses in man. The genome and proteins of this  
 CC virus can be used in gene therapy and vaccination against the virus,  
 CC which also causes disorders of the gastrointestinal tract, including  
 CC Crohn's disease and lupus erythematosus, inflammatory diseases, and  
 CC proliferative disorders such as cancer  
 XX  
 SQ Sequence 278 BP; 83 A; 67 C; 53 G; 75 T; 0 U; 0 Other;  
 Query Match 68.2%; Score 15; DB 3; Length 278;  
 Best Local Similarity 100.0%; Pred. No. 99;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 GTACCACCTGGTCTTC 16  
 DB 28 GTACCACCTGGTCTTC 14  
 RESULT 10  
 AAH92754  
 ID AAH92754 standard; DNA; 700 BP.  
 XX  
 AC AAH92754;  
 XX  
 DT 09-OCT-2001 (first entry)  
 XX  
 DE Human inflammatory bowel disease related gene fragment IGR3079a.  
 XX  
 KW Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;  
 KW single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;  
 KW chromosome 5q31-33; forensic test; gene therapy; ds.  
 XX  
 OS Homo sapiens.  
 XX





CC the efficacy of a therapy for inhibiting prostate cancer in a patient;  
CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)  
CC determining whether prostate cancer has metastasized in a patient; (h)  
CC assessing the aggressiveness or indolence of prostate cancer in a patient  
CC ; (i) is also useful as a pharmacodynamic or pharmacogenomic marker  
XX  
SQ Sequence 823 BP; 299 A; 162 C; 201 G; 160 T; 0 U; 1 Other;

Query Match 68.2%; Score 15; DB 5; Length 823;  
Best Local Similarity 100.0%; Pred. No. 97;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTGGCTTCTTGTGC 22  
Db 717 CTGGCTTCTTGTGC 703

## RESULT 13

AAC45720  
ID AAC45720 standard; DNA; 1076 BP.

XX AC AAC45720;

XX DT 18-OCT-2000 (first entry)

XX DE Arabidopsis thaliana DNA fragment SEQ ID NO: 47521.

XX KW Hybridisation assay; genetic mapping; gene expression control;  
XX KW protein identification; signal transduction pathway; metabolic pathway;  
XX KW promoter; termination sequence; ss.

XX OS Arabidopsis thaliana.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-00301439.

XX PR 25-FEB-1999; 99US-0121825P.

XX PR 05-MAR-1999; 99US-0121825P.

XX PR 09-MAR-1999; 99US-0123548P.

XX PR 23-MAR-1999; 99US-0125788P.

XX PR 29-MAR-1999; 99US-0126264P.

XX PR 01-APR-1999; 99US-0126785P.

XX PR 06-APR-1999; 99US-0127462P.

XX PR 08-APR-1999; 99US-0128234P.

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PR 29-OCT-1999; 99US-0162142P.

Query Match 68.2%; Score 15; DB 3; Length 1078;  
Best Local Similarity 100.0%; Pred. No. 96;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TACACTGGCTCTCT 17

Db 279 TACCACTGGTCTTCT 293  
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ID AAX97978 standard; DNA; 1267 BP.  
XX  
XX  
XX AC AAX97978;  
XX  
XX DT 17-SEP-1999 (first entry)  
XX  
XX DE Human secreted protein gene 63.  
XX  
XX KW Human; secreted protein; cancer; tumour; developmental abnormality;  
KW foetal deficiency; blood disorder; immune system disorder; inflammation;  
KW autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;  
KW schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;  
KW atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;  
KW digestive disorder; endocrine disorder; infection; AIDS; ss.  
XX  
XX OS Homo sapiens.  
XX  
XX EN WO931117-A1.  
XX  
XX PD 24-JUN-1999.  
XX  
XX PF 17-DEC-1998; 98WO-US027059.  
XX  
XX PR 18-DEC-1997; 97US-0068006P.  
XX PR 18-DEC-1997; 97US-0068007P.  
XX PR 18-DEC-1997; 97US-0068008P.  
XX PR 18-DEC-1997; 97US-00680053P.  
XX PR 18-DEC-1997; 97US-00680054P.  
XX PR 18-DEC-1997; 97US-00680057P.  
XX PR 18-DEC-1997; 97US-00680064P.  
XX PR 18-DEC-1997; 97US-0070923P.  
XX PR 18-DEC-1997; 97US-0068169P.  
XX PR 19-DEC-1997; 97US-0068365P.  
XX PR 19-DEC-1997; 97US-0068367P.  
XX PR 19-DEC-1997; 97US-0068368P.  
XX PR 19-DEC-1997; 97US-0068369P.  
XX  
XX PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX PI Moore PA, Ruben SM, Carter KC, Shi Y, Rosen CA, Soppet DR;  
XX PI Kyaw H, Wei Y, Florence K, Duan RD, Florence C, Greene JM, Feng P;  
XX PI Perrie AM, Yu G, Janat F, Ni J;  
XX  
XX DR WPI: 1999-418749/35.  
XX DR P-PSDB; AAY36286.  
XX  
XX PT New isolated human genes encoding secreted polypeptides.  
XX  
XX PS Claim 1; Page 309; 537pp; English.  
XX  
XX CC AAX97916 to AAX98029 represent 110 isolated human secreted protein genes.  
XX CC AAX36224 to AAY36727 represent the secreted proteins encoded by the 110  
XX CC human genes. The genes and their corresponding secreted polypeptides are  
XX CC useful for preventing, treating or ameliorating medical conditions, e.g.  
XX CC by protein or gene therapy. Also pathological conditions can be diagnosed  
XX CC by determining the amount of the new polypeptides in a sample or by  
XX CC determining the presence of mutations in the new genes. Specific uses are  
XX CC described for each of the 110 genes, based on which tissues they are most  
XX CC highly expressed in, and include developing products for the diagnosis or  
XX CC treatment of cancer, tumours, developmental abnormalities and foetal  
XX CC deficiencies, blood disorders, diseases of the immune system, autoimmune  
XX CC diseases, inflammation, allergies, Alzheimer's and cognitive disorders,  
XX CC schizophrenia, arthritis, asthma, psoriasis, sepsis, skin disorders,  
XX CC atherosclerosis, diabetes, cardiovascular disorders, kidney disorders,  
XX CC digestive/endocrine disorders, infections and AIDS. The polypeptides are  
XX CC also useful for identifying their binding partners. The sequences given  
XX CC in AAX97907 to AAX97915 and AAY36223 are used in the exemplification of

CC the present invention  
XX Sequence 1267 BP; 329 A; 311 C; 344 G; 283 T; 0 U; 0 Other;  
SQ  
Query Match 68.2%; Score 15; DB 2; Length 1267;  
Best Local Similarity 100.0%; Pred. NO. 96;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 CACTGGTCTTCTTGT 20  
|||||  
Db 45 CACTGGTCTTCTTGT 31  
Search completed: August 2, 2004, 18:24:24  
Job time : 109.207 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 2, 2004, 17:27:15 ; Search time 492,914 Seconds  
(without alignments)  
1934.510 Million cell updates/sec

Title: US-10-068-067-17  
Perfect score: 22  
Sequence: 1 ggtaccactggtcttctgtgc 22

Scoring table: OLIGO.NUC  
Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_hgt.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sv.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_on.\*
- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pl.\*
- 26: em\_ro.\*
- 27: em\_sts.\*
- 28: em\_un.\*
- 29: em\_vi.\*
- 30: em\_hgt\_hum.\*
- 31: em\_hgt\_inv.\*
- 32: em\_hgt\_other.\*
- 33: em\_hgt\_mus.\*
- 34: em\_hgt\_pln.\*
- 35: em\_hgt\_rtd.\*
- 36: em\_hgt\_mam.\*
- 37: em\_hgt\_vrt.\*
- 38: em\_sv.\*
- 39: em\_hgo\_hum.\*
- 40: em\_hgo\_mus.\*
- 41: em\_hgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	22	100.0	22	6	AX513218	Sequence
2	22	100.0	51	6	AX513217	Sequence
3	22	100.0	51	6	AX513222	Sequence
4	22	100.0	348	9	AF262299	Homo sapi
5	22	100.0	957	9	AF224496	Homo sapi
6	22	100.0	1453	9	AF247360	Homo sapi
7	22	100.0	1454	9	AF247359	Homo sapi
8	22	100.0	2895	6	AX513212	Sequence
9	22	100.0	2895	9	AF237380	Homo sapi
10	22	100.0	177334	9	AC138069	Homo sapi
11	22	100.0	19279	9	AC104439	Homo sapi
12	22	100.0	220965	2	HS312688	Homo sapi
13	21	95.5	21	6	AX513223	Sequence
14	19	86.4	260	9	AF224495	Homo sapi
15	19	86.4	406	9	AF262301	Homo sapi
16	19	86.4	410	9	AF262302	Homo sapi
17	18	81.8	212	9	AF262303	Homo sapi
18	18	81.8	436	9	AF262304	Homo sapi
19	18	81.8	173554	2	AC144357	Danio rer
20	17	77.3	5883	2	AC129517	Homo sapi
21	17	77.3	112182	2	AC141177	Rattus no
22	17	77.3	114458	10	BX293986	Mouse DNA
23	17	77.3	161826	9	AL358532	Human DNA
24	17	77.3	172834	2	AC135133	Rattus no
25	17	77.3	172834	2	AC011277	Homo sapi
26	17	77.3	196769	2	AC120900	Rattus no
27	17	77.3	204102	2	AC013826	Homo sapi
28	17	77.3	202220	2	AC125657	Rattus no
29	17	77.3	229200	2	AC106425	Rattus no
30	17	77.3	235201	2	AC114470	Rattus no
31	17	77.3	240230	2	AC094364	Rattus no
32	17	77.3	248921	2	AC095538	Rattus no
33	17	77.3	264110	2	AC122626	Rattus no
34	16	72.7	2052	6	AX838677	Sequence
35	16	72.7	2052	6	AX838678	Sequence
36	16	72.7	2209	6	AX838628	Sequence
37	16	72.7	2209	6	AX838629	Sequence
38	16	72.7	3052	6	AX838676	Sequence
39	16	72.7	42925	9	AL844165	Human DNA
40	16	72.7	110000	2	AC134360	Continuation (2 of
41	16	72.7	146575	2	AC135571	Rattus no
42	16	72.7	152908	10	AC130550	Mus muscu
43	16	72.7	185227	2	BX248245	Danio rer
44	16	72.7	185564	5	BX088530	Zebrafish
45	16	72.7	171221	2	AC034255	Mus muscu

ALIGNMENTS

RESULT 1  
AX513218  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

AX513218  
Sequence 17 from Patent WO02062848.  
AX513218  
AX513218.1 GI:23504281  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.  
Rotherberg, M.E. and Zimmerman, N.  
Regulation of cc chemokine receptor 3 (ccr3) expression  
Patent: WO 02062848-A 17 15-AUG-2002;

AX513218  
22 bp  
DNA  
linear  
PAT 03-OCT-2002

## CHILDREN'S HOSPITAL MEDICAL CENTER (US)

## FEATURES

source  
Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
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## ORIGIN

Query Match 100.0%; Score 22; DB 6; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.022; 0; Indels 0; Gaps 0;  
Matches 22; Conservative 0; Mismatches 0;

QY 1 GGTACCACTGGTCTTCTGTGC 22  
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DB 1 GGTACCACTGGTCTTCTGTGC 22

## RESULT 2

AX513217 AX513217 51 bp DNA linear PAT 03-OCT-2002  
DEFINITION Sequence 16 from Patent WO02062848.  
ACCESSION AX513217  
VERSION AX513217.1 GI:23504280

## KEYWORDS

SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 Rothenberg M.E. and Zimmerman, N.

AUTHORS Regulation of cc chemokine receptor 3 (ccr3) expression

TITLE Patent: WO 02062848-A 16 15-AUG-2002;

JOURNAL CHILDREN'S HOSPITAL MEDICAL CENTER (US)

## FEATURES

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Location/Qualifiers  
1..51  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

## ORIGIN

Query Match 100.0%; Score 22; DB 6; Length 51;  
Best Local Similarity 100.0%; Pred. No. 0.021; 0; Indels 0; Gaps 0;  
Matches 22; Conservative 0; Mismatches 0;

QY 1 GGTACCACTGGTCTTCTGTGC 22  
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DB 1 GGTACCACTGGTCTTCTGTGC 22

## RESULT 3

AX513222 AX513222 51 bp RNA linear PAT 03-OCT-2002  
DEFINITION Sequence 21 from Patent WO02062848.  
ACCESSION AX513222  
VERSION AX513222.1 GI:23504285

## KEYWORDS

SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 Rothenberg M.E. and Zimmerman, N.

AUTHORS Regulation of cc chemokine receptor 3 (ccr3) expression

TITLE Patent: WO 02062848-A 21 15-AUG-2002;

JOURNAL CHILDREN'S HOSPITAL MEDICAL CENTER (US)

## FEATURES

source  
Location/Qualifiers  
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/mol\_type="unassigned RNA"  
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## ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.021;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACCACTGGTCTTCTGTGC 22  
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DB 1 GGTACCACTGGTCTTCTGTGC 22

## RESULT 4

AF262299 AF262299 348 bp mRNA linear PRI 26-JUN-2002  
LOCUS Homo sapiens clone 1 CC chemokine receptor 3 (CCR3) mRNA, partial  
DEFINITION cds.

ACCESSION AF262299

VERSION AF262299.1 GI:19171640

## KEYWORDS

SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 348)

AUTHORS Vijh, S., Dayhoff, D.E., Wang, C.E., Imam, Z., Ehrenberg, P.K. and

Michael, N.L.

TITLE Transcription Regulation of Human Chemokine Receptor CCR3: Evidence

for a Rare TATA-less Promoter Structure Conserved between

Drosophila and Humans

JOURNAL Genomics 80 (1), 86-95 (2002)

MEDLINE 22074933

PUBMED 12079287

REFERENCE 2 (bases 1 to 348)

AUTHORS Vijh, S., Dayhoff, D.E., Wang, C.E., Ehrenberg, P.K. and Michael, N.L.

TITLE Direct Submission

JOURNAL Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis,

Walter Reed Army Institute of Research, 1600 E. Gude Drive,

Rockville, MD 20850, USA

## FEATURES

source  
Location/Qualifiers  
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/clone="1"  
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/gene="CCR3"  
120..>348  
/gene="CCR3"  
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## gene

## CDS

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/protein\_id="AAU85628.1"  
/db\_xref="GI:19171641"  
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FTVGLLGNVVVMILIKYRLRINTNTIYLLN"

## ORIGIN

Query Match 100.0%; Score 22; DB 9; Length 348;  
Best Local Similarity 100.0%; Pred. No. 0.017;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACCACTGGTCTTCTGTGC 22  
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DB 27 GGTACCACTGGTCTTCTGTGC 48

## RESULT 5

AF24496S1 AF24496S1 957 bp DNA linear PRI 02-MAY-2001  
LOCUS Homo sapiens CC chemokine receptor 3 (CCR3) gene, exon 1.  
DEFINITION

ACCESSION AF224496  
 VERSION AF224496.1 GI:13924485  
 KEYWORDS  
 SEGMENT 1 of 2  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 957)  
 AUTHORS Scotet,E.J.  
 TITLE CCR3 expression is associated with chromatin remodeling in Th2 cells  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 957)  
 AUTHORS Scotet,E.J.  
 TITLE Direct Submission  
 JOURNAL Submitted (13-JAN-2000) Basel Institute for Immunology, 487  
 Grenzachstrasse, Basel CH-4005, Switzerland  
 FEATURES  
 source 1..957  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 exon 298..376  
 /gene="CCR3"  
 /note="exon 1"  
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 Best Local Similarity 100.0%; Pred. No. 0.016;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGTACCACTGGTCTTCTGTGC 22  
 |||||  
 DB 295 GGTACCACTGGTCTTCTGTGC 316  
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 RESULT 6  
 AF247360 1453 bp DNA linear PRI 26-JUN-2002  
 LOCUS Homo sapiens CC chemokine receptor 3 (CCR3) gene, promoter region  
 DEFINITION and partial sequence.  
 ACCESSION AF247360  
 VERSION AF247360.1 GI:19110541  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1453)  
 AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and Michael,N.L.  
 TITLE Transcription Regulation of Human Chemokine Receptor CCR3: Evidence for a Rare TATA-less Promoter Structure Conserved between Drosophila and Humans  
 JOURNAL Genomics 80 (1), 86-95 (2002)  
 MEDLINE 22074933  
 PUBMED 12079287  
 REFERENCE 2 (bases 1 to 1453)  
 AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.  
 TITLE Direct Submission  
 JOURNAL Submitted (21-MAR-2000) Dept. of Mol. Diag. and Pathogenesis, U.S. Military HIV Research Program, 1600 E. Gude Drive, Rockville, MD 20850, USA  
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 /clone="A8"  
 /cell\_type="peripheral blood mononuclear cell"

Gene 1..>1453  
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 Best Local Similarity 100.0%; Pred. No. 0.015; 0; Gaps 0;  
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 QY 1 GGTACCACTGGTCTTCTGTGC 22  
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 DB 1082 GGTACCACTGGTCTTCTGTGC 1103  
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 RESULT 7  
 AF247359 1454 bp DNA linear PRI 26-JUN-2002  
 LOCUS Homo sapiens CC chemokine receptor 3 (CCR3) gene, promoter region  
 DEFINITION and partial sequence.  
 ACCESSION AF247359  
 VERSION AF247359.1 GI:19110540  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1454)  
 AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and Michael,N.L.  
 TITLE Transcription Regulation of Human Chemokine Receptor CCR3: Evidence for a Rare TATA-less Promoter Structure Conserved between Drosophila and Humans  
 JOURNAL Genomics 80 (1), 86-95 (2002)  
 MEDLINE 22074933  
 PUBMED 12079287  
 REFERENCE 2 (bases 1 to 1454)  
 AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.  
 TITLE Direct Submission  
 JOURNAL Submitted (21-MAR-2000) Dept. of Mol. Diag. and Pathogenesis, U.S. Military HIV Research Program, 1600 E. Gude Drive, Rockville, MD 20850, USA  
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 /clone="A7"  
 /cell\_type="peripheral blood mononuclear cell"  
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 mRNA 823..>1454  
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 exon 823..1164  
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## ORIGIN

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 Matches 22; Conservative 0;

Qy 1 GGTACCACTGGTCTTCTTGTC 22  
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Db 1083 GGTACCACTGGTCTTCTTGTC 1104  
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RESULT 8  
 AX513212 2895 bp DNA linear PAT 03-OCT-2002  
 LOCUS AX513212  
 DEFINITION Sequence 11 from Patent WO02062848.  
 ACCESSION AX513212  
 VERSION AX513212.1 GI:23504275

SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
 Rothenberg, M.E. and Zimmerman, N.  
 Regulation of cc chemokine receptor 3 (ccr3) expression  
 Patent: WO 02062848-A 11 15-AUG-2002;  
 CHILDREN'S HOSPITAL MEDICAL CENTER (US)

FEATURES  
 source 1..2895  
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## ORIGIN

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Qy 1 GGTACCACTGGTCTTCTTGTC 22  
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Db 1561 GGTACCACTGGTCTTCTTGTC 1582  
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RESULT 9  
 AF237380S1 2895 bp DNA linear PRI 05-OCT-2000  
 LOCUS AF237380S1  
 DEFINITION Homo sapiens CCR3 gene, promoter and exon 1.  
 ACCESSION AF237380  
 VERSION AF237380.1 GI:10643652

SEGMENT 1 of 2  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
 (bases 1 to 2895)  
 Daugherty, B.L., Daugherty, B.L., Kavannah, J.L., El-Awar, F.Y.,  
 Zimmerman, N.A. and Rothenberg, M.E.  
 Analysis of the CC chemokine receptor 3 gene reveals a complex 5'  
 exon organization, a functional role for untranslated exon 1, and a  
 broadly active promoter with eosinophil-selective elements  
 Blood 96 (7), 2346-2354 (2000)

JOURNAL MEDLINE 20458773  
 PUBMED 11001881

REFERENCE 2 (bases 1 to 2895)

Daugherty, B.L.

Direct Submission

TITLE Submitted (22-FEB-2000) Immunology & Rheumatology, Merck Research  
 Laboratories, 126 East Lincoln Avenue, Rahway, NJ 07065, USA  
 Location/Qualifiers

FEATURES  
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 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"

/db\_xref="taxon:9606"

/chromosome="3"

/map="3p21"

/clone="350-38"

/clone\_lib="BgIII fragment from phase I human genomic  
 library (DMPC-HFF No. 1; Genome Systems, Inc., St. Louis,  
 MO)"

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/gene="CCR3"

33..38

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1287..1292

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1552..1642

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## ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 0.014;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTACCACTGGTCTTCTTGTC 22  
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Db 1561 GGTACCACTGGTCTTCTTGTC 1582  
 |||||

RESULT 10  
 AC138069 177334 bp DNA linear PRI 19-FEB-2003  
 LOCUS AC138069  
 DEFINITION Homo sapiens chromosome 3 clone RP13-546I2, complete sequence.  
 ACCESSION AC138069  
 VERSION AC138069.3 GI:28416170

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 177334)  
 Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,  
 Saenphimmachak, C., Buckley, D., Kibukawa, M., Raymond, C. and  
 Haugen, E.D.

REFERENCE 1  
 Direct Submission  
 Unpublished  
 2 (bases 1 to 177334)  
 Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.  
 Direct Submission  
 Submitted (12-DEC-2002) Genome Center, University of Washington,  
 Box 352145, Seattle, WA 98195, USA

REFERENCE 3 (bases 1 to 177334)

Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.

Direct Submission

Submitted (10-JAN-2003) Genome Center, University of Washington,  
 Box 352145, Seattle, WA 98195, USA

REFERENCE 4 (bases 1 to 177334)

Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,  
 Saenphimmachak, C., Buckley, D., Kibukawa, M., Raymond, C. and  
 Haugen, E.D.

Direct Submission

Submitted (19-FEB-2003) Genome Center, University of Washington,  
 Box 352145, Seattle, WA 98195, USA

On Feb 19, 2003 this sequence version replaced gi:27573398.

----- Genome Center

Center: University of Washington Genome Center

Center Code: UWGC

Web site: http://www.genome.washington.edu

Contact: uwgchgsu@u.washington.edu

----- Project Information

Center project name: chr-3

Center clone name: RP13-546I2 (bc0820)

----- Summary Statistics

Sequencing vector: plasmid; 100% of reads



Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.990319  
 Consensus quality: 177210 bases at least Q40  
 Consensus quality: 177313 bases at least Q30  
 Consensus quality: 177334 bases at least Q20  
 Insert size: 177334; sum-of-contigs  
 Quality coverage: 9.3x in Q20 bases; sum-of-contigs

#### Overlapping Sequences:

5': RP11-793E15 (UMGC:bc0564) AC104439, 95469-bp overlap  
 3': U95626, 42710-bp overlap

#### Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

#### Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

#### HindIII

#### EcoRI

#### BglII

SeqDerMap	FngPrnt	SeqDerMap	FngPrnt	SeqDerMap	FngPrnt
1239	1199	11125	10952	6306	6319
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510	<800	560	<800	3913	3756
6511	6363	54	<800	2169	2210
5296	5509	1159	1158	910	910
10424	10027	4052	4034	875	883
5046	5119	1846	1829	3716	3756
1196	1199	8334	8273	4502	4523
1397	1392	12882	12573	1967	1945
2597	2624	448	<800	2864	2871
1688	1674	12737	12573	4724	4738
3800	3818	10300	10103	4773	4738
2248	2269	6671	6656	3707	3756

1074	1055	4052	4034	336	<800
7303	7718	1392	1386	79	<800
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551	<800	2791	2834	1889	1945
1074	1055	2647	2682	3696	3756
5688	5759	3423	3409	1569	1539
5183	5363	73	<800	8078	8038
3100	3093	499	<800	1365	1325
921	959	723	<800	289	<800
4350	4244	2763	2834	11047	10790
4931	4857	6594	6656	8848	8963
3907	3818	4503	4468	1914	1945
8001	7718	5154	5136	1336	1325
3804	3818	4730	4713	11485	11341
2355	2376	13628	13324	974	975
862	868	166	<800	2448	2501
1711	1674	9554	9494	373	<800
5672	5759	1398	1386	1003	975
3900	3818	1613	1641	1787	1756
1905	1854	1479	1503	857	883
7872	7718	1540	1503	1974	1945
1174	1155	520	<800	1707	1631
7015	7139	219	<800	3835	3756
2852	2868	1571	1503	6586	6551
221	<800	154	<800	178	<800
1002	1055	5077	5136	2905	2871
201	<800	2156	2190	2500	2501
6717	6864	1075	1089	389	<800
237	<800	162	<800	41	<800
2737	2749	2752	2834	685	<800
3448	3416	1647	1641	2598	2662
3256	3238	7059	7056	248	<800
5801	5759	1547	1503	2152	2210
1512	1497	5163	5136	431	<800
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8413	8333	2033	2035	3380	3411
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1026 1055 <800
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14333 14484 3144
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10701 10790
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1321 1325
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Best Local Similarity 100.0%; Pred. No. 0.0094; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACCACCTGGTCTTCTTGTGC 22
|||||
Db 65693 GGTACCACCTGGTCTTCTTGTGC 65714

RESULT 11
AC104439
LOCUS Homo sapiens chromosome 3 clone RP11-793E15, complete sequence.
AC104439 AC024739
AC104439.2 GI:21490240
VERSION HTG.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 197279)
AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
Saenphimmachak,C., Phelps,K.A., Buckley,D., Kibukawa,M., Raymond,C.
and Haugen,E.D.
Direct Submission
Unpublished
2 (bases 1 to 197279)
Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.
Direct Submission
Submitted (11-DEC-2001) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
3 (bases 1 to 197279)
Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
Saenphimmachak,C., Phelps,K.A., Buckley,D., Kibukawa,M., Raymond,C.
and Haugen,E.D.
Direct Submission
Submitted (20-JUN-2002) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
On Jun 20, 2002 this sequence version replaced gi:17488621.
-----
Center: University of Washington Genome Center
Center Code: UWGC
Web site: http://www.genome.washington.edu
Contact: uwgctgseq.washington.edu
Drafting Center: WUGSC
-----
Project Information
Center project name: chr-3
Center clone name: RP11-793E15 (bc0564)
-----
Summary Statistics
Sequencing vector: unknown; 52% of reads
Sequencing vector: plasmid; L08752; 48% of reads
Chemistry: Dye-terminator ET; 94% of reads
Chemistry: Dye-terminator Big Dye; 6% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 197168 bases at least Q40
Consensus quality: 197255 bases at least Q30
Consensus quality: 197275 bases at least Q20
Insert size: 197279; sum-of-contigs
Quality coverage: 8.2x in Q20 bases; sum-of-contigs
Overlapping Sequences:

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5': RP11-91E8 (UWGC:bc0216) AC026349  
3': CTD-2563A18 (UWGC:bc0730)

# Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the Genbank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

# Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

HindIII			BglII			EcoRI			
SeqDerMap	FrgrPrint	SeqDerMap	FrgrPrint	SeqDerMap	FrgrPrint	SeqDerMap	FrgrPrint	SeqDerMap	FrgrPrint
2687	2617	8949	8586	8696	8661				
6382	6410	2067	2160	6	<800				
512	<800	7846	7940	2742	2803				
449	<800	3734	3895	5376	5324				
2602	2763	1334	1301	1493	1478				
2590	2617	2287	2309	823	835				
8313	8291	1814	1918	1962	2002				
1711	1683	691	<800	2900	2954				
9821	9472	5477	5348	1484	1478				
516	<800	305	<800	1005	995				
8587	8291	25245	25541	1181	1171				
7446	7581	3988	4121	18560	19002				
2088	2075	1633	1598	3603	3579				
2509	2617	631	<800	4943	5076				
3519	3501	90	<800	3239	3241				
26	<800	402	<800	953	995				
925	933	3350	3490	1621	1615				
98	<800	4577	4515	6827	6900				

6409	6410	1183	79	<800
1383	1376	4331	16418	16263
16048	15829	4121	3361	3241
1876	1877	2497	872	881
4169	4068	<800	4220	4193
1674	1683	2309	2848	2803
52	<800	11045	2283	2318
5227	5082	5632	3211	3241
15464	15829	1414	4615	4632
14333	14296	<800	6823	6900
1026	1026	3895	886	881
645	<800	1414	2032	2002
6621	6410	2497	8680	8661
8413	8291	<800	5163	5076
1401	1376	2012	1547	1478
1512	1471	<800	7058	6900
5801	5644	21003	1647	1615
3256	3278	3666	2753	2803
3448	3501	1301	162	<800
2738	2763	10502	1078	1093
237	<800	3317	2156	2173
6715	6823	<800	5077	5076
201	<800	3490	154	<800
1002	1026	5632	1571	1478
221	<800	3317	219	<800
2854	2899	<800	520	<800
6998	7317	<800	1540	1478
1174	1145	2160	1479	1478
7876	8291	<800	1613	1615
1911	1877	2778	1399	1478
3899	3847	<800	9553	9383
5672	5644	<800	166	<800
1711	1683	<800	13615	13115
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Query Match 100.0%; Score 22; DB 9; Length 197279;  
 Best Local Similarity 100.0%; Pred. No. 0.0093;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTACCACTGGTCTTCTTGTC 22

Db 167486 GGTACCACTGGTCTTCTTGTC 167507

# RESULT 12

LOCUS HSA312688

DEFINITION Homo sapiens chromosome 3 clone RP6-32g23 map 3p21.3, \*\*\*

ACCESSION AJ312688.2

VERSION AJ312688.2

KEYWORDS HTG; HTGS PHASE2.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Kiss, H., Yang, X., Kiss, C., Andersson, K., Klein, G., Imreh, S. and

Dumanski, J.P.

TITLE The transcriptional map of the common eliminated region 1 (C3CER1)

JOURNAL Eur. J. Hum. Genet. 10 (1), 52-61 (2002)

MEDLINE 21906202

PUBMED 11896456

REFERENCE 2 (bases 1 to 220965)

AUTHORS Kiss, H.

TITLE Direct Submission

JOURNAL Submitted (01-APR-2001) Kiss H., Microbiology and Tumorbiology

Center (MTC), Karolinska Institute, Box 280, Stockholm, S-17177,

SWEDEN

COMMENT On Apr 5, 2001 this sequence version replaced gi:13548633.

The sequence is a consensus sequence of clone RP4-787c23 (1-140400

bp),

clone RP6-32g23 (31212-220965 bp), clone RP6-146e1 (partially,

1-6800 bp)

and clone RP6-188g11 (partially, 1-108303 bp). The sequencing

contigs are

in order and the gaps between them are represented by 100 Ns.

Contig 1:

1-11731 bp

Contig 2: 11832-26218 bp

Contig 3: 26319-28347 bp

Contig 4:

28448-42160 bp

Contig 5: 42261-55059 bp

Contig 6: 55160-61578 bp

Contig 7: 61679-97342 bp

Contig 8: 97443-117655 bp

Contig 9:

117756-118727 bp

Contig 10: 118828-121834 bp

Contig 11: 121935-127855 bp

Contig 12:

127956-129383 bp

Contig 13: 129484-131747 bp

Contig 14:

131848-132316 bp

Contig 15: 132417-134455 bp

Contig 16: 134556-135527 bp

Contig 17:

135628-189051 bp

Contig 18: 189152-189476 bp

Contig 19:

189577-191375 bp

Contig 20: 191476-201473 bp

Contig 21: 201574-202307 bp

Contig 22:

202408-204878 bp

Contig 23: 204979-213531 bp

Contig 24:

213632-218109 bp

Contig 25: 218210-219800 bp

Contig 26: 219901-220965 bp.

\* NOTE: This is a 'working draft' sequence. It currently

\* consists of 26 contigs. Gaps between the contigs

\* are represented as runs of N. The order of the pieces

\* is believed to be correct as given, however the sizes

\* of the gaps between them are based on estimates that have

\* provided by the submitter.  
 \* This sequence will be replaced  
 \* by the finished sequence as soon as it is available and  
 \* the accession number will be preserved.

1 11731: contig of 11731 bp in length  
 \* 11732 11831: gap of 100 bp  
 \* 11832 26218: contig of 14387 bp in length  
 \* 26219 26318: gap of 100 bp  
 \* 26319 28347: contig of 2029 bp in length  
 \* 28348 28448: gap of 100 bp  
 \* 28449 42160: contig of 13713 bp in length  
 \* 42161 42360: gap of 200 bp  
 \* 42361 55059: contig of 12699 bp in length  
 \* 55060 55159: gap of 100 bp  
 \* 55160 61578: contig of 6419 bp in length  
 \* 61579 61678: gap of 100 bp  
 \* 61679 97342: contig of 35664 bp in length  
 \* 97343 97442: gap of 100 bp  
 \* 97443 117655: contig of 20213 bp in length  
 \* 117656 117755: gap of 100 bp  
 \* 117756 118727: contig of 972 bp in length  
 \* 118728 118827: gap of 100 bp  
 \* 118828 121834: contig of 3007 bp in length  
 \* 121835 121935: gap of 100 bp  
 \* 121936 127955: contig of 5921 bp in length  
 \* 127956 129383: contig of 1428 bp in length  
 \* 129384 129483: gap of 100 bp  
 \* 129484 131747: contig of 2264 bp in length  
 \* 131748 131847: gap of 100 bp  
 \* 131848 132316: contig of 469 bp in length  
 \* 132317 132416: gap of 100 bp  
 \* 132417 134455: contig of 2039 bp in length  
 \* 134456 134556: gap of 100 bp  
 \* 134557 135527: contig of 972 bp in length  
 \* 135528 135627: gap of 100 bp  
 \* 135628 189051: contig of 53424 bp in length  
 \* 189052 189151: gap of 100 bp  
 \* 189152 189476: contig of 325 bp in length  
 \* 189477 189576: gap of 100 bp  
 \* 189577 191375: contig of 1799 bp in length  
 \* 191376 191475: gap of 100 bp  
 \* 191476 201473: contig of 9998 bp in length  
 \* 201474 201573: gap of 100 bp  
 \* 201574 202307: contig of 734 bp in length  
 \* 202308 202407: gap of 100 bp  
 \* 202408 204878: contig of 2471 bp in length  
 \* 204879 204979: gap of 100 bp  
 \* 204980 213531: contig of 8553 bp in length  
 \* 213532 213631: gap of 100 bp  
 \* 213632 218109: contig of 4478 bp in length  
 \* 218110 218209: gap of 100 bp  
 \* 218210 219800: contig of 1591 bp in length  
 \* 219801 219900: gap of 100 bp  
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 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTACCACTGGTCTCTCTGTGC 22

Db 121110 GGTACCACTGGTCTCTCTGTGC 121131

## RESULT 13

AX513223  
 LOCUS  
 DEFINITION Sequence 22 from Patent WO02062848.  
 ACCESSION AX513223  
 VERSION AX513223.1 GI:23504286  
 KEYWORDS Homo sapiens (human)  
 SOURCE  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 Rothenberg M.E. and Zimmerman N.  
 Regulation of cc chemokine receptor 3 (ccr3) expression  
 Patent: WO 02062848-A 22 15-AUG-2002;  
 CHILDREN'S HOSPITAL MEDICAL CENTER (US)  
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 Best Local Similarity 100.0%; Pred. No. 0.09;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTACCACTGGTCTCTCTGTG 21

Db 1 GGTACCACTGGTCTCTCTGTG 21

## RESULT 14

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 LOCUS  
 DEFINITION Homo sapiens CC chemokine receptor 3 (CCR3) mRNA, partial cds.  
 ACCESSION AF224495  
 VERSION AF224495.1 GI:13924481  
 KEYWORDS Homo sapiens (human)  
 SOURCE  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (Bases 1 to 260)  
 Scotet, E.J.  
 CCR3 expression is associated with chromatin remodeling in Th2  
 cells  
 Unpublished  
 2 (bases 1 to 260)  
 Scotet, E.J.  
 Direct Submission  
 TITLE Submitted (13-JAN-2000) Basel Institute for Immunology, 487  
 Grenzacherstrasse, Basel CH-4005, Switzerland  
 JOURNAL  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
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## CDS

## ORIGIN

Query Match 86.4%; Score 19; DB 9; Length 260;

Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ACCACTGGTCTCTTTGTGC 22  
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Db 1 ACCACTGGTCTCTTTGTGC 19

## RESULT 15

AF262301  
LOCUS 406 bp mRNA linear PRI 26-JUN-2002  
DEFINITION Homo sapiens clone 4 CC chemokine receptor 3 (CCR3) mRNA, partial  
cds.

ACCESSION AF262301  
VERSION AF262301.1 GI:19171644

SOURCE Homo sapiens (human)  
ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 406)

REFERENCE Vijs, S., Dayhoff, D.E., Wang, C.E., Inam, Z., Ehrenberg, P.K. and  
Michael, N.L.  
TITLE Transcription Regulation of Human Chemokine Receptor CCR3: Evidence  
for a Rare TATA-Less Promoter Structure Conserved between  
Drosophila and Humans

JOURNAL Genomics 80 (1), 86-95 (2002)  
MEDLINE 22074933  
PubMed 12079287

REFERENCE 2 (bases 1 to 406)  
AUTHORS Vijs, S., Dayhoff, D.E., Wang, C.E., Ehrenberg, P.K. and Michael, N.L.  
TITLE Direct Submission  
JOURNAL Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis,  
Walter Reed Army Institute of Research, 1600 E. Gude Drive,  
Rockville, MD 20850, USA

## FEATURES

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## CDS

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## ORIGIN

Query Match 86.4%; Score 19; DB 9; Length 406;

Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ACCACTGGTCTCTTTGTGC 22  
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Db 1 ACCACTGGTCTCTTTGTGC 19

Search completed: August 2, 2004, 19:07:52  
Job time : 494.914 secs

***This Page Blank (uspto)***

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 2, 2004, 18:10:40 ; Search time 22.1897 Seconds  
(without alignments)  
550.208 Million cell updates/sec

Title: US-10-068-067-17

Perfect score: 22  
Sequence: 1 ggtaccactggtctcttctgtgc 22

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA.\*

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3: /cgn2\_6/ptodata/2/ina/6A COMB.seq:\*  
4: /cgn2\_6/ptodata/2/ina/6B COMB.seq:\*  
5: /cgn2\_6/ptodata/2/ina/PCTUS COMB.seq:\*  
6: /cgn2\_6/ptodata/2/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	68.2	3177	3	US-09-134-513-1
2	15	68.2	118067	4	US-08-497-855A-32
3	14	63.6	495	4	US-09-621-976-17953
4	14	63.6	508	4	US-09-621-976-3046
5	14	63.6	542	4	US-09-669-751-135
6	14	63.6	698	4	US-09-634-238-126
7	14	63.6	865	4	US-09-640-419C-6
8	14	63.6	1760	4	US-09-495-050A-139
9	14	63.6	2114	4	US-08-370-838-158
10	14	63.6	3142	1	US-08-110-158-3
11	14	63.6	3142	4	US-09-023-655-1090
12	14	63.6	3144	5	PCT-US91-05059-1
13	14	63.6	3812	1	US-08-188-582-19
14	14	63.6	3812	1	US-08-646-715-19
15	13	59.1	21	4	US-09-422-978-9067
16	13	59.1	285	4	US-08-313-294A-1150
17	13	59.1	698	3	US-08-998-416-756
18	13	59.1	882	4	US-09-543-681A-1777
19	13	59.1	914	4	US-09-673-395A-114
20	13	59.1	1104	4	US-09-252-991A-13171
21	13	59.1	1152	4	US-09-461-325-38
22	13	59.1	1152	4	US-10-012-542-38
23	13	59.1	1301	4	US-08-489-847-108
24	13	59.1	1308	4	US-09-205-258-215
25	13	59.1	1457	4	US-09-673-395A-554
26	13	59.1	1457	4	US-09-673-395A-554
27	13	59.1	1471	4	US-09-620-312D-446

Sequence 3779, Ap  
Sequence 12780, A  
Sequence 11, Appl  
Sequence 8, Appl  
Sequence 6, Appl  
Sequence 20, Appl  
Sequence 20, Appl  
Sequence 20, Appl  
Sequence 20, Appl  
Sequence 48, Appl  
Sequence 1298, Ap  
Sequence 18, Appl  
Sequence 22, Appl  
Sequence 37, Appl  
Sequence 3185, Ap  
Sequence 11, Appl  
Sequence 2, Appl  
Sequence 2, Appl

US-09-328-352-3779  
US-09-252-991A-12780  
US-09-591-095-11  
US-09-782-906-8  
US-09-782-906-6  
US-09-620-312D-800  
US-08-420-235B-20  
US-08-793-624-20  
PCT-US95-10194-20  
US-09-205-258-48  
US-09-489-039A-1298  
US-09-445-041-18  
US-09-078-972A-22  
US-09-282-147-37  
US-09-134-000C-3185  
US-10-164-595-11  
US-09-248-571-2  
US-09-553-736-2

#### ALIGNMENTS

RESULT 1  
US-09-134-513-1  
; Sequence 1, Application US/09134513  
; Patent No. 6210964  
; GENERAL INFORMATION:  
; APPLICANT: Brown, Edward M.  
; APPLICANT: Diaz, Ruben  
; APPLICANT: Bai, Mei  
; APPLICANT: Quinn, Stephen J.  
; TITLE OF INVENTION: The Avian Extracellular Calcium-Sensing  
; TITLE OF INVENTION: Receptor  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Vinson & Elkins L.L.P.  
; STREET: 1455 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.  
; ZIP: 20004-1008  
; COMPUTER: IBM PC compatible  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09134,513  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sanzo, Michael A.  
; REGISTRATION NUMBER: 36,912  
; REFERENCE/DOCKET NUMBER: BR1331/13003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)639-6585  
; TELEFAX: (202)639-6604  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3177 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHEICAL: NO  
US-09-134-513-1

Query Match 68.2%; Score 15; DB 3; Length 3177;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTGCTCTTCTGTGC 22





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; SEQ ID NO 126
; LENGTH: 698
; TYPE: DNA
; ORGANISM: Lactobacillus rhamnosus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(698)
; OTHER INFORMATION: n = A,T,C or G
US-09-634-238-126

Query Match      63.6%; Score 14; DB 4; Length 698;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 TGGTCTCTCTGTGC 22
Db 550 TGGTCTCTCTGTGC 563

RESULT 7
US-09-640-419C-6/c
; Sequence 6, Application US/09640419C
; Patent No. 6830615
; GENERAL INFORMATION:
; APPLICANT: Bidney, Dennis L
; APPLICANT: Crasta, Oswald R
; APPLICANT: Hu, Xu
; APPLICANT: Lu, Guihua
; TITLE OF INVENTION: DEFENSE-RELATED SIGNALING GENES AND METHODS OF USE
; FILE REFERENCE: 35718/199009 (5718-92)
; CURRENT APPLICATION NUMBER: US/09/640.419C
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,656
; PRIOR FILING DATE: 1999-08-18
; PRIOR APPLICATION NUMBER: 60/206,405
; PRIOR FILING DATE: 2000-05-23
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 865
; TYPE: DNA
; ORGANISM: Helianthus annuus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(519)
US-09-640-419C-6

Query Match      63.6%; Score 14; DB 4; Length 865;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CTGGTCTCTCTGTG 21
Db 129 CTGGTCTCTCTGTG 116

RESULT 8
US-09-495-050A-139/c
; Sequence 139, Application US/09495050A
; Patent No. 6492505
; GENERAL INFORMATION:
; APPLICANT: Roopa, Reddy
; APPLICANT: Guegler, Karl, J.
; APPLICANT: Au-young, Janice
; TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED P
; FILE REFERENCE: PA-0013 US
; CURRENT APPLICATION NUMBER: US/09/495,050A
; CURRENT FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/118,318
; PRIOR FILING DATE: February 1, 1999
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: PERL Program
; SEQ ID NO 139
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; LENGTH: 1760
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6492505 1518320CT1
US-09-495-050A-139

Query Match      63.6%; Score 14; DB 4; Length 1760;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CTGGTCTCTCTGTG 21
Db 1432 CTGGTCTCTCTGTG 1419

RESULT 9
US-09-370-838-158
; Sequence 158, Application US/09370838
; Patent No. 6444425
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Roadoh
; APPLICANT: Secret, Heather
; TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
; FILE REFERENCE: 210121.475C1
; CURRENT APPLICATION NUMBER: US/09/370,838
; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: US 09/285,323
; EARLIER FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 289
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 158
; LENGTH: 2114
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-370-838-158

Query Match      63.6%; Score 14; DB 4; Length 2114;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTACCACCTGGTCT 14
Db 1463 GGTACCACCTGGTCT 1476

RESULT 10
US-08-110-158-3/c
; Sequence 3, Application US/08110158
; Patent No. 5605821
; GENERAL INFORMATION:
; APPLICANT: McEver, Rodger P.
; APPLICANT: Pan, Junliang
; TITLE OF INVENTION: Expression Control Sequences of the
; TITLE OF INVENTION: P-Selectin Gene
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 1100 Peachtree Street, Suite 2800
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-4530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/110,158
; FILING DATE: 19930820
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/320,408
; FILING DATE: 08-MAR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-815-6508
; TELEFAX: (404)-815-6555
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3142 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-110-158-3

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Query Match 63.6%; Score 14; DB 1; Length 3142;  
 Best Local Similarity 100.0%; Pred. No. 46;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      8 CTGGTCTTCTTG 21
      |||||
Db      2822 CTGGTCTTCTTG 2809

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RESULT 11
US-09-023-655-1090/c
; Sequence 1090, Application US/09023655
; Patent No 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1090:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3142 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

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; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 9183390
US-09-023-655-1090

Query Match 63.6%; Score 14; DB 4; Length 3142;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 CTGGTCTTCTTG 21
      |||||
Db      2822 CTGGTCTTCTTG 2809

RESULT 12
PCT-US91-05059-1/c
; Sequence 1, Application PC/TUS9105059
; GENERAL INFORMATION:
; APPLICANT: Regents of the Board of the, University of
; APPLICANT: Oklahoma
; TITLE OF INVENTION: Functionally Active Selectin-Derived
; TITLE OF INVENTION: Peptides
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kilpatrick & Cody
; STREET: 100 Peachtree Street, Suite 3100
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: US
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/05059
; FILING DATE: 19910717
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/320408
; FILING DATE: 08-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/554199
; FILING DATE: 17-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMRF110CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-572-6508
; TELEFAX: 404-572-6555
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3144 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; PRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapien
; TISSUE TYPE: Blood
; CELL TYPE: Endothelial
; FEATURE:
; NAME/KEY: polyA signal
; LOCATION: 2833..2838
; OTHER INFORMATION: /note= "Potential polyadenylation
; OTHER INFORMATION: signals"
; FEATURE:

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; NAME/KEY: polyA signal  
; LOCATION: 3124..3130  
; OTHER INFORMATION: /note="Potential polyadenylation  
; OTHER INFORMATION: signal"  
PCT-US91-05059-1

Query Match 63.6%; Score 14; DB 5; Length 3144;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTGGTCTTCTTG 21  
|||||

DB 2822 CTGGTCTTCTTG 2809

## RESULT 13

US-08-188-582-19/c  
; Sequence 19, Application US/08188582  
; Patent No. 5534410  
; GENERAL INFORMATION:  
; APPLICANT: Tjian, Robert  
; APPLICANT: Comai, Lucio  
; APPLICANT: Dynlacht, Brian D.  
; APPLICANT: Hoey, Timothy  
; APPLICANT: Ruppert, Siegfried  
; APPLICANT: Tanese, Naoko  
; APPLICANT: Wang, Edith  
; APPLICANT: Weinzierl, Robert O.J.  
; TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,  
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFs AND METHODS OF USE  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT  
; STREET: 4 Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-4187  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/188,582  
; FILING DATE: 28-JAN-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Osman, Richard A  
; REGISTRATION NUMBER: 36,627  
; REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO  
; TELEPHONE: (415) 781-1989  
; TELEFAX: (415) 398-3249  
; TELEX: 910 277299  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3812 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 60..3701  
US-08-188-582-19

Query Match 63.6%; Score 14; DB 1; Length 3812;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CACTGGTCTTCTTG 19  
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DB 3126 CACTGGTCTTCTTG 3113

## RESULT 14

US-08-646-715-19/c  
; Sequence 19, Application US/08646715  
; Patent No. 5637686  
; GENERAL INFORMATION:  
; APPLICANT: Tjian, Robert  
; APPLICANT: Comai, Lucio  
; APPLICANT: Dynlacht, Brian D.  
; APPLICANT: Hoey, Timothy  
; APPLICANT: Ruppert, Siegfried  
; APPLICANT: Tanese, Naoko  
; APPLICANT: Wang, Edith  
; APPLICANT: Weinzierl, Robert O.J.  
; TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,  
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFs AND METHODS OF USE  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT  
; STREET: 4 Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-4187  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/646,715  
; FILING DATE: 09-MAY-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/188,582  
; FILING DATE: 28-JAN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Osman, Richard A  
; REGISTRATION NUMBER: 36,627  
; REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO  
; TELEPHONE: (415) 781-1989  
; TELEFAX: (415) 398-3249  
; TELEX: 910 277299  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3812 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 60..3701  
US-08-646-715-19

Query Match 63.6%; Score 14; DB 1; Length 3812;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CACTGGTCTTCTTG 19  
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DB 3126 CACTGGTCTTCTTG 3113

## RESULT 15

US-09-422-978-9067  
; Sequence 9067, Application US/09422978  
; Patent No. 6537751  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Daniel

; APPLICANT: Blumenfeld, Marta  
; APPLICANT: Chumakov, Ilya  
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...  
; FILE REFERENCE: GENSET.020CP1  
; CURRENT APPLICATION NUMBER: US/09/422,978  
; CURRENT FILING DATE: 1999-10-20  
; EARLIER APPLICATION NUMBER: US 09/298,850  
; EARLIER FILING DATE: 1999-04-21  
; EARLIER APPLICATION NUMBER: US 60/109,732  
; EARLIER FILING DATE: 1998-11-23  
; EARLIER APPLICATION NUMBER: US 60/082,614  
; EARLIER FILING DATE: 1998-04-21  
; NUMBER OF SEQ ID NOS: 11796  
; SEQ ID NO 9067  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: primer\_bind  
; LOCATION: 1..21  
; OTHER INFORMATION: downstream amplification primer 99-2170 for SEQ 1202, in compleme  
US-09-422-978-9067

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Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GGTCCTCTTGTGC 13

Search completed: August 2, 2004, 20:30:03  
Job time : 23.1897 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 2, 2004, 18:06:45 ; Search time 909.207 Seconds

(without alignments)

722.573 Million cell updates/sec

Title: US-10-068-067-17

Perfect score: 22

Sequence: 1 ggtaccactgctctcttctgtgc 22

Scoring table:

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Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	17	77.3	613	28	BH299085
C 2	17	77.3	905	10	BF340232
C 3	16	72.7	221	10	BF557219
C 4	16	72.7	224	9	AA957733

C 5	16	72.7	322	10	AW826871
C 6	16	72.7	346	12	BG738607
C 7	16	72.7	364	10	BF389025
C 8	16	72.7	406	9	AI112888
C 9	16	72.7	422	13	EX307267
C 10	16	72.7	433	14	CB495381
C 11	16	72.7	433	14	CB495414
C 12	16	72.7	433	14	CB495567
C 13	16	72.7	451	13	BY505647
C 14	16	72.7	456	10	BF388753
C 15	16	72.7	500	10	BF402543
C 16	16	72.7	522	10	BE831025
C 17	16	72.7	552	12	BJ057835
C 18	16	72.7	569	29	CE396889
C 19	16	72.7	601	14	CB495211
C 20	16	72.7	624	28	AQ744376
C 21	16	72.7	674	12	BI296051
C 22	16	72.7	677	14	CB499837
C 23	16	72.7	700	29	AG138506
C 24	16	72.7	723	9	AU056819
C 25	16	72.7	742	29	AG059138
C 26	16	72.7	744	29	CG957943
C 27	16	72.7	766	29	CG675256
C 28	16	72.7	797	28	BZ122800
C 29	16	72.7	832	10	BF246442
C 30	16	72.7	838	14	CK017521
C 31	16	72.7	846	28	BZ215165
C 32	16	72.7	882	10	BF300865
C 33	16	72.7	918	29	CNS051G8
C 34	16	72.7	944	29	CNS04H92
C 35	16	72.7	1053	28	CC283410
C 36	16	72.7	1117	12	BG829094
C 37	15	68.2	121	12	BQ034576
C 38	15	68.2	172	14	CK104844
C 39	15	68.2	174	12	BI005360
C 40	15	68.2	201	29	AL755014
C 41	15	68.2	297	10	BE523740
C 42	15	68.2	319	13	BY151693
C 43	15	68.2	330	13	EX635885
C 44	15	68.2	342	12	EM386785
C 45	15	68.2	359	10	BE688637

#### ALIGNMENTS

RESULT 1  
BH299085/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BH299085 613 bp DNA linear GSS 30-NOV-2001  
CH230-146H22.TJ CHORI-230 Segment 1 Rattus norvegicus genomic clone  
CH230-146H22, genomic survey sequence.  
BH299085  
BH299085.1 GI:17211493  
GSS.  
Rattus norvegicus (Norway rat)  
Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
1 (bases 1 to 613)  
Zhao,S., Shetty,J., Shatsman,S., Tsengye,G., Geer,K.,  
Shvartsbeyn,A., Gebregorgis,E., Overton,L., Russell,D., Chen,D.,  
Riggs,F., de Jong,P. and Fraser,C.M.  
Rat BAC End Sequences from Library CHORI-230 EcoRI segment  
Unpublished (1999)  
Other GSSs: CH230-146H22.TV  
Contact: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: szhao@tigr.org

AW826871 fk54a12.Y  
BG738607 fp60f09.Y  
BF389025 UI-R-BS2-  
AI112888 UI-R-YO-m  
EX307267 EX307267  
CB495381 omykswel0  
CB495414 omykswel0  
CB495567 omykswel0  
BY505647 BY505647  
BF388753 UI-R-BS2-  
BF402543 UI-R-CAO-  
BE831025 PM2-MT003  
BJ057835 BJ057835  
CE396889 tigr-gss-  
CB495211 omykgrh00  
AQ744376 HS\_5502.A  
BI296051 UI-R-DK0-  
CB499837 ssalrkc0  
AG138506 Pan trogl  
AU056819 AU056819  
AG059138 Pan trogl  
CG957943 MBEIO81TF  
CG675256 trs2988.t  
BZ122800 CH230-318  
BF246442 601821506  
CK017521 AGENCOURT  
BZ215165 CH230-250  
CC283410 CH261-138  
BG829094 602752438  
BQ034576 1091004D0  
CK104844 1059F41.5  
BI005360 CM0-HN020  
AL755014 Arabidops  
BE523740 M41B11STM  
BY151693 BY151693  
EX635885 EX635885  
EM386785 UI-R-CNI-  
BE688637 uw37h02.X

Clones are derived from the rat BAC library CHORI-230 (<http://www.chori.org/bacpac/rat230.htm>). For BAC library availability, please contact Pieter de Jong (pdejong@mail.choi.org). Clones may be purchased from BACPAC Resources ([http://www.chori.org/bacpac/or\\_xing\\_information.htm](http://www.chori.org/bacpac/or_xing_information.htm)). BAC end page: [http://www.tigr.org/tdb/bac\\_ends/rat/bac\\_end\\_intro.html](http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html)  
 Plate: 146 row: H column: 22  
 Seq primer: SP6  
 Class: BAC ends.

## FEATURES

Location/Qualifiers  
 1. .613  
 /organism="Rattus norvegicus"  
 /mol\_type="genomic DNA"  
 /strain="BN/SsNHsd/MCW"  
 /db\_xref="taxon:10116"  
 /clone="CH230-146H22"  
 /sex="female"  
 /cell\_type="Brain"  
 /clone\_lib="CHORI-230 Segment 1"  
 /notes="Vector: PTABAC2.1; Site 1: EcoRI; Site 2: EcoRI;  
 CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by  
 Pieter de Jong"

## ORIGIN

Query Match 77.3%; Score 17; DB 28; Length 613;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCACTGGTCTCTCTGTG 21  
 |||||  
 Db 172 CCACTGGTCTCTCTGTG 156

## RESULT 2

BF340232/c 905 bp mRNA linear EST 22-NOV-2000  
 LOCUS 602036821F1 NCI\_CGAP\_Brn64 Homo sapiens cDNA clone IMAGE:4184908  
 DEFINITION 5', mRNA sequence.

ACCESSION BF340232  
 VERSION BF340232.1 GI:11286694  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens  
 Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 905)  
 NIH-MGC <http://mgs.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgapsb@mail.nih.gov](mailto:cgapsb@mail.nih.gov)  
 Tissue Procurement: David N. Louis, M.D.  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: L1AM9503 row: 1 column: 05  
 High quality sequence stop: 675.

## FEATURES

Location/Qualifiers  
 1. .905  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4184908"  
 /tissue\_type="glioblastoma with EGFR amplification"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /clone\_lib="NCI CGAP Brn64"  
 /notes="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;  
 Site 2: SalI. Cloned unidirectionally. Primer: oligo dr.  
 Average insert size 1.57 kb. Constructed by Life  
 Technologies. Note: this is a NCI\_CGAP Library."

## ORIGIN

Query Match 77.3%; Score 17; DB 10; Length 905;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ACCACTGGTCTCTCTGT 20  
 |||||  
 Db 674 ACCACTGGTCTCTCTGT 658

## RESULT 3

BF557219 221 bp mRNA linear EST 12-DEC-2000  
 LOCUS UI-R-E1-gc-b-11-0-UI-r1 UI-R-E1 Rattus norvegicus cDNA clone  
 DEFINITION UI-R-E1-gc-b-11-0-UI 5', mRNA sequence.

ACCESSION BF557219  
 VERSION BF557219.1 GI:11666949  
 KEYWORDS EST.

## ORGANISM

Rattus norvegicus (Norway rat)  
 Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.

## REFERENCE

1 (bases 1 to 221)  
 Bonaldo,M.F., Lennon,G. and Soares,M.B.  
 AUTHORS Normalization and subtraction: two approaches to facilitate gene  
 TITLE discovery  
 JOURNAL Genome Res. 6 (9), 791-806 (1996)  
 MEDLINE 97044477  
 PUBMED 889548

## COMMENT

Contact: Soares, MB  
 Coordinated Laboratory for Computational Genomics  
 University of Iowa  
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: [bento-soares@uiowa.edu](mailto:bento-soares@uiowa.edu)  
 CDNA Library Preparation: M.B. Soares Lab Clone distribution:  
 clones will be available through Research Genetics ([www.resgen.com](http://www.resgen.com))  
 This clone is also available through the I.M.A.G.E. Consortium at  
 LLNL ([info@image.llnl.gov](mailto:info@image.llnl.gov)). IMAGE ID= 1772378  
 Seq primer: M13 Forward.

## FEATURES

Location/Qualifiers  
 1. .221  
 /organism="Rattus norvegicus"  
 /mol\_type="mRNA"  
 /strain="Sprague-Dawley"  
 /db\_xref="taxon:10116"  
 /clone="UI-R-E1-gc-b-11-0-UI"  
 /dev\_stage="adult"  
 /lab\_host="DH10B (Life Technologies)"  
 /clone\_lib="UI-R-E1"  
 /notes="Vector: pT73D-Pac (Pharmacia) with a modified  
 polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-E1  
 library is a subtracted library derived from the UI-R-E0  
 library. The UI-R-E0 library consisted of a mixture of  
 individually tagged normalized libraries constructed from  
 8, 12 and 18-day embryo. The tag is a string of 3-5  
 nucleotides present between the Not I site and the  
 oligo-dr track which allows identification of the library  
 of origin of a clone within the mixture. The subtracted  
 library (UI-R-E1) was constructed as follows: PCR  
 amplified cDNA inserts from a pool of UI-R-E0 clones from  
 which 3' ESTs had been derived was used as a driver in a  
 hybridization with the UI-R-E0 library in the form of  
 circles (subtracted library). The remaining single-stranded  
 hydroxyapatite column chromatography, converted to  
 double-stranded circles and electroporated into DH10B  
 bacteria (Life Technologies) to generate the UI-R-E1  
 library. This procedure has been previously described  
 (Bonaldo, Lennon and Soares, Genome Research 6: 791-806,

1996")

## ORIGIN

Query Match 72.7%; Score 16; DB 10; Length 221;  
 Best Local Similarity 100.0%; Pred. No. 6.5e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CACTGCTCTCTGTG 21

Db 93 CACTGCTCTCTGTG 108

## RESULT 4

AA957733/c  
 LOCUS 224 bp mRNA linear EST 04-JUL-1999  
 DEFINITION UI-R-E1-gc-b-11-0-UI.s1 UI-R-E1 Rattus norvegicus cDNA clone  
 UI-R-E1-gc-b-11-0-UI 3', mRNA sequence.

ACCESSION AA957733

VERSION AA957733.1 GI:4277623

KEYWORDS EST.

SOURCE Rattus norvegicus (Norway rat)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus

1 (bases 1 to 224)

Bonaldo, M.F., Lennon, G. and Soares, M.B.

Normalization and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

9704477

889548

On May 7, 1998 this sequence version replaced gi:3121428.

Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

The sequence tag present in the cDNA between the NotI site and the  
 oligo-dT track served to identify it as a clone from the normalized  
 adult 18-day-embryo library. cDNA Library Preparation: M. Fatima  
 Bonaldo, Ph.D. clone distribution: clones will be available through  
 Research Genetics This clone is also available through the  
 I.M.A.G.E. Consortium at LLNL (info@image.llnl.gov). IMAGE

ID=1772378

Seq primer: M13 Forward

PODFA=No.

## FEATURES

source

Location/Qualifiers  
 1..224  
 /organism="Rattus norvegicus"  
 /mol\_type="mRNA"  
 /strain="Sprague-Dawley"  
 /db\_xref="taxon:10116"  
 /clone="UI-R-E1-gc-b-11-0-UI"  
 /dev\_stage="adult"  
 /lab\_host="DH10B (Life Technologies)"  
 /clone\_lib="UI-R-E1"  
 /note="Vector: pUT73D-Pac (Pharmacia) with a modified  
 polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-E1  
 library is a subtracted library derived from the UI-R-E0  
 library. The UI-R-E0 library consisted of a mixture of  
 individually tagged normalized libraries constructed from  
 8, 12 and 18-day embryo. The tag is a string of 3-5  
 nucleotides present between the Not I site and the  
 oligo-dT track which allows identification of the library  
 of origin of a clone within the mixture. The subtracted  
 library (UI-R-E1) was constructed as follows: PCR  
 amplified cDNA inserts from a pool of UI-R-E0 clones from  
 which 3' ESTs had been derived was used as a driver in a  
 hybridization with the UI-R-E0 library in the form of  
 single-stranded circles. The remaining single-stranded

circles (subtracted library) was purified by  
 hydroxyapatite column chromatography, converted to  
 double-stranded circles and electroporated into DH10B  
 bacteria (Life Technologies) to generate the UI-R-E1  
 library. This procedure has been previously described  
 (Bonaldo, Lennon and Soares, Genome Research 6: 791-806,  
 1996)"

## ORIGIN

Query Match 72.7%; Score 16; DB 9; Length 224;  
 Best Local Similarity 100.0%; Pred. No. 6.5e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CACTGCTCTCTGTG 21

Db 129 CACTGCTCTCTGTG 114

## RESULT 5

AW826871/c  
 LOCUS 322 bp mRNA linear EST 13-FEB-2002  
 DEFINITION FX54a12.y1 zebrafish adult retina cDNA Danio rerio cDNA 5' similar  
 to FR:042104 042104 ARRESTIN.1, mRNA sequence.

ACCESSION AW826871

VERSION AW826871.1 GI:7919948

KEYWORDS EST.

SOURCE Danio rerio (zebrafish)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
 Cypriniformes; Cyprinidae; Danio

1 (bases 1 to 322)

Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M.,

Bady, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, F.,

Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,

Persson, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,

Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,

Waterston, R. and Wilson, R.

WashU Zebrafish EST Project 1998

Unpublished (1998)

Contact: Stephen L. Johnson

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: zbrafish@watson.wustl.edu

Library constructed by: Chandra Tucker and Gregory Niemi DNA  
 Sequencing by: Washington University Genome Sequencing Center Clone  
 distribution: RessourcenzentrumPrimatDatenbank, Berlin, Germany  
 (web address: www.rzpd.de)

Seq primer: T3 ET from Amersham

Trace considered overall poor quality

High quality sequence stop: 1.

## FEATURES

source

Location/Qualifiers  
 1..322  
 /organism="Danio rerio"  
 /mol\_type="mRNA"  
 /strain="wild-type"  
 /db\_xref="taxon:7955"  
 /sex="mixed"  
 /dev\_stage="1-2 years"  
 /lab\_host="E.Coli XL1-Blue MRF" (XL1-Blue MRF)"  
 /clone\_lib="Zebrafish adult retina cDNA"  
 /note="Vector: Lambda ZAP II (phagescript SK-); Site 1:  
 EcoRI; Site 2: SalI; This Zebrafish library was  
 constructed by Dr. Susan B. Brockerhoff (email:  
 sbrockers@u.washington.edu) RZPD library number: 760"

## ORIGIN

Query Match 72.7%; Score 16; DB 10; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 6.6e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCACTGGTCTTCTGT 20  
 |||||  
 Db 30 CCACTGGTCTTCTGT 15

## RESULT 6

BG738607/c

LOCUS

DEFINITION

fp60f09.y1 Zebrafish adult retina cDNA Danio rerio cDNA clone  
 IMAGE:4786337 5' similar to TR:042104 O42104 ARRESTIN. ; mRNA  
 sequence.

ACCESSION

BG738607

VERSION

BG738607.1

KEYWORDS

EST.

SOURCE

Danio rerio (zebrafish)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
 Cypriniformes; Cyprinidae; Danio.

REFERENCE

AUTHORS

Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M.,  
 Eddy, S., Hillier, L., Kucabara, J., Martin, J., Beck, C., Wyllie, J.,  
 Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,  
 Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,  
 Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,  
 Waterston, R., and Wilson, R.

TITLE

WashU Zebrafish EST Project 1998

JOURNAL

Unpublished (1998)

COMMENT

Contact: Stephen L. Johnson  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810

Email: zbrafish@wustl.edu

Library constructed by: Chandra Tucker and Gregory Niemi DNA  
 Sequencing by: Washington University Genome Sequencing Center Clone  
 distribution: Ressourcenzentrum Primatdatenbank, Berlin, Germany  
 (web address: www.rzpd.de)

Trace considered overall poor quality

Seq primer: T3 ET from Amersham

High quality sequence stop: 1.

FEATURES

source

1. 346  
 Location/Qualifiers  
 /organism="Danio rerio"  
 /mol\_type="mRNA"  
 /strain="wild-type"  
 /db\_xref="taxon:7955"  
 /clone="IMAGE:4786337"  
 /sex="mixed"  
 /dev\_stage="1-2 years"  
 /lab\_host="E.Coli XL1-Blue MRF' (XL1-Blue MRF')"  
 /clone\_lib="Zebrafish adult retina cDNA"  
 /notes="Vector: Lambda ZAP II (pBluescript SK-); Site\_1:  
 EcoRI; Site\_2: SalI; This Zebrafish library was  
 constructed by Dr. Susan E. Brockerhoff (email:  
 sbrocker@u.washington.edu) RZPD library number: 760"

ORIGIN

Query Match

Best Local Similarity

Matches

16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCACTGGTCTTCTGT 20

|||||

Db 24 CCACTGGTCTTCTGT 9

RESULT 7

BF389025/c

LOCUS

DEFINITION

UI-R-BS2-bdk-h-10-0-UI.s1 UI-R-BS2 Rattus norvegicus cDNA clone  
 UI-R-BS2-bdk-h-10-0-UI 3', mRNA sequence.

ACCESSION

BF389025

VERSION

KEYWORDS

SOURCE

ORGANISM

Rattus norvegicus (Norway rat)

REFERENCE

AUTHORS

TITLE

Normalization and subtraction: two approaches to facilitate gene

discovery

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

The sequence contained an oligo-dT track that was present in the

oligonucleotide that was used to prime the synthesis of first

strand cDNA and therefore this may represent a Bonafide poly A

tail. The sequence tag present in the cDNA between the NotI site

and the oligo-dT track served to verify it as a clone from the

normalized embryo at 13 dpc library cDNA Library Preparation: M.B.

Soares Lab Clone distribution: clones will be available through

Research Genetics (www.resgen.com)

Seq primer: M13 Forward

POLYA=Yes.

FEATURES

source

1. 364

Location/Qualifiers

/organism="Rattus norvegicus"

/mol\_type="mRNA"

/strain="Sprague-Dawley"

/db\_xref="taxon:10116"

/clone="UI-R-BS2-bdk-h-10-0-UI"

/dev\_stage="embryonic 13 dpc"

/lab\_host="DH10B (Life Technologies)"

/clone\_lib="UI-R-BS2"

/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified

polylinker; Site\_1: Not I; Site\_2: Eco RI; The UI-R-BS2

library is a subtracted library derived from 13 dpc whole

embryo tissue. For a detailed description of the library

from which this clone was derived, please visit our web

site at ratest.eng.uiowa.edu. The subtraction has been

previously described in (Bonaldo, Lennon and Soares,

Genome Research 6:791-806, 1996)

TAG\_TISSUE=embryo at 13 dpc

TAG\_LIB=UI-R-BS2

TAG\_SEQ=AATCC"

ORIGIN

Query Match

Best Local Similarity

Matches

16; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

QY 6 CACTGGTCTTCTGTG 21

|||||

Db 129 CACTGGTCTTCTGTG 114

RESULT 8

A112888/c

LOCUS

DEFINITION

UI-R-Y0-mj-g-07-0-UI.s1 UI-R-Y0 Rattus norvegicus cDNA clone

UI-R-Y0-mj-g-07-0-UI 3', mRNA sequence.

ACCESSION

A112888

VERSION

A112888.1

KEYWORDS

EST.

SOURCE

Rattus norvegicus (Norway rat)

ORGANISM

Rattus norvegicus

BF389025.1

GI:11373852

EST.

Rattus norvegicus (Norway rat)

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (bases 1 to 364)

Bonaldo, M.F., Lennon, G. and Soares, M.B.

Normalization and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

97044477

8889548

Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

The sequence contained an oligo-dT track that was present in the

oligonucleotide that was used to prime the synthesis of first

strand cDNA and therefore this may represent a Bonafide poly A

tail. The sequence tag present in the cDNA between the NotI site

and the oligo-dT track served to verify it as a clone from the

normalized embryo at 13 dpc library cDNA Library Preparation: M.B.

Soares Lab Clone distribution: clones will be available through

Research Genetics (www.resgen.com)

Seq primer: M13 Forward

POLYA=Yes.

FEATURES

Location/Qualifiers

1. 364

/organism="Rattus norvegicus"

/mol\_type="mRNA"

/strain="Sprague-Dawley"

/db\_xref="taxon:10116"

/clone="UI-R-BS2-bdk-h-10-0-UI"

/dev\_stage="embryonic 13 dpc"

/lab\_host="DH10B (Life Technologies)"

/clone\_lib="UI-R-BS2"

/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified

polylinker; Site\_1: Not I; Site\_2: Eco RI; The UI-R-BS2

library is a subtracted library derived from 13 dpc whole

embryo tissue. For a detailed description of the library

from which this clone was derived, please visit our web

site at ratest.eng.uiowa.edu. The subtraction has been

previously described in (Bonaldo, Lennon and Soares,

Genome Research 6:791-806, 1996)

TAG\_TISSUE=embryo at 13 dpc

TAG\_LIB=UI-R-BS2

TAG\_SEQ=AATCC"

ORIGIN

Query Match

Best Local Similarity

Matches

16; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

QY 6 CACTGGTCTTCTGTG 21

|||||

Db 129 CACTGGTCTTCTGTG 114

RESULT 8

A112888/c

LOCUS

DEFINITION

UI-R-Y0-mj-g-07-0-UI.s1 UI-R-Y0 Rattus norvegicus cDNA clone

UI-R-Y0-mj-g-07-0-UI 3', mRNA sequence.

ACCESSION

A112888

VERSION

A112888.1

KEYWORDS

EST.

SOURCE

Rattus norvegicus (Norway rat)

ORGANISM

Rattus norvegicus

406 bp mRNA linear EST 11-FEB-1999

UI-R-Y0-mj-g-07-0-UI.s1 UI-R-Y0 Rattus norvegicus cDNA clone

UI-R-Y0-mj-g-07-0-UI 3', mRNA sequence.

A112888

A112888

A112888.1

GI:3512837

Rattus norvegicus (Norway rat)

Rattus norvegicus



Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE  
1 (bases 1 to 406)  
Bonaldo,M.F., Lennon,G. and Soares,M.B.  
Normalization and subtraction: two approaches to facilitate gene discovery

JOURNAL  
MEDLINE  
PUBMED  
COMMENT

Genome Res. 6 (9), 791-806 (1996)  
97044477  
8889548  
Contact: Soares, MB  
Coordinated Laboratory for Computational Genomics  
University of Iowa  
375 Newton Road  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: bento-soares@uiowa.edu  
The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized adult Eye library. cDNA Library Preparation: M. Fatima Bonaldo, Ph.D. Clone distribution: clones will be available through Research Genetics

Seq primer: M13 Forward.  
Location/Qualifiers  
1..406  
/organism="Rattus norvegicus"  
/mol\_type="mRNA"  
/strain="Sprague-Dawley"  
/db\_xref="taxon:10116"  
/clones="UI-R-Y0-mj-g-07-0-UI"  
/dev\_stage="adult"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_libs="UI-R-Y0"  
/note="Vector: pMT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-Y0 library is a subtracted library derived from an individually-tagged normalized whole-eye (minus the lens) library. The driver for the subtraction consisted of a pool of all previous libraries (UI-R-A0, UI-R-A1, UI-R-E0, UI-R-E1, UI-R-C0, and UI-R-C1). The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-Y0) was constructed as follows: PCR amplified cDNA inserts from previous library clones from which 3' ESTs had been derived were used as a driver in a hybridization with the normalized whole-eye library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-Y0 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996).

# FEATURES

Location/Qualifiers

1..406

/organism="Rattus norvegicus"

/mol\_type="mRNA"

/strain="Sprague-Dawley"

/db\_xref="taxon:10116"

/clones="UI-R-Y0-mj-g-07-0-UI"

/dev\_stage="adult"

/lab\_host="DH10B (Life Technologies)"

/clone\_libs="UI-R-Y0"

/note="Vector: pMT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-Y0 library is a subtracted library derived from an individually-tagged normalized whole-eye (minus the lens) library. The driver for the subtraction consisted of a pool of all previous libraries (UI-R-A0, UI-R-A1, UI-R-E0, UI-R-E1, UI-R-C0, and UI-R-C1). The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-Y0) was constructed as follows: PCR

amplified cDNA inserts from previous library clones from which 3' ESTs had been derived were used as a driver in a hybridization with the normalized whole-eye library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-Y0 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996).

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amplified cDNA inserts from previous library clones from which 3' ESTs had been derived were used as a driver in a hybridization with the normalized whole-eye library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-Y0 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996).

amplified cDNA inserts from previous library clones from which 3' ESTs had been derived were used as a driver in a hybridization with the normalized whole-eye library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-Y0 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996).

amplified cDNA inserts from previous library clones from which 3' ESTs had been derived were used as a driver in a hybridization with the normalized whole-eye library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-Y0 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996).

amplified cDNA inserts from previous library clones from which 3' ESTs had been derived were used as a driver in a hybridization with the normalized whole-eye library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-Y0 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996).

# VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

EX307267.1 GI:29587912  
EST.  
Oncorhynchus mykiss (rainbow trout)  
Oncorhynchus mykiss  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus. 1 (bases 1 to 422)  
Govoroun,M., Guiguen,Y. and Le Gac,F.  
Construction and primary characterization of normalized cDNA libraries in rainbow trout, Oncorhynchus mykiss  
Unpublished (2003)  
Contact: Guiguen Y  
INRA - SCRIBE  
Campus de Beaulieu, RENNES cedex, 35042, France  
Tel: 02.23.48.50.09  
Fax: 02.23.48.50.20  
Email: Yann.Guiguen@beaulieu.rennes.inra.fr  
Sequence cleaned of vector, adaptor and repetitions. Contact us at sigenasupport@jouy.inra.fr to obtain the chromatogram of this sequence.  
Plate: 0017 row: d column: 6  
Seq primer: M13R.  
Location/Qualifiers  
1..422  
/organism="Oncorhynchus mykiss"  
/mol\_type="mRNA"  
/db\_xref="taxon:8022"  
/clone="tcay0017b.d.06"  
/tissue\_type="adipose tissue, blood, brain, kidney, liver, muscle, ovary, pituitary, testis"  
/dev\_stage="from embryos to adults"  
/lab\_host="DH10B"  
/clone\_libs="AGENAE Rainbow trout multi-tissues subtracted library (tcay)"  
/note="Vector: pMT73D-pac; Rainbow trout multi-tissues - normalized + 1 subtraction (tcay); Clone distribution : AGENAE Resource centre, Francois PIUMI, Francois.piumi@jouy.inra.fr, INRA, CEA Radiobiologie et Etude du genome (IREG), Domaine de Vilvert, 78352, Jouy-en-Josas cedex, FRANCE"

# FEATURES

source

Location/Qualifiers

1..422

/organism="Oncorhynchus mykiss"

/mol\_type="mRNA"

/db\_xref="taxon:8022"

/clone="tcay0017b.d.06"

/tissue\_type="adipose tissue, blood, brain, kidney, liver, muscle, ovary, pituitary, testis"

/dev\_stage="from embryos to adults"

/lab\_host="DH10B"

/clone\_libs="AGENAE Rainbow trout multi-tissues subtracted library (tcay)"

/note="Vector: pMT73D-pac; Rainbow trout multi-tissues - normalized + 1 subtraction (tcay); Clone distribution : AGENAE Resource centre, Francois PIUMI, Francois.piumi@jouy.inra.fr, INRA, CEA Radiobiologie et Etude du genome (IREG), Domaine de Vilvert, 78352, Jouy-en-Josas cedex, FRANCE"

# ORIGIN

Query Match 72.7%; Score 16; DB 13; Length 422;  
Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CACTGGTCTCTTGTG 21

Db 223 CACTGGTCTCTTGTG 238

# RESULT 10

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

CB495381 433 bp mRNA linear EST 27-MAR-2003  
omykswel006018 Oncorhynchus mykiss Chilliack River steelhead whole  
Oncorhynchus mykiss cDNA, mRNA sequence.  
CB495381  
CB495381.1 GI:29306607  
EST.  
Oncorhynchus mykiss (rainbow trout)  
Oncorhynchus mykiss  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus. 1 (bases 1 to 433)  
GRASP Consortium, Davidson,W.S., Koop,B.F. and  
http://web.uvic.ca/cbr/grasp.  
A survey of Salmo salar transcripts from high complexity cDNA  
Unpublished (2002)  
Contact: Koop BF

Centre for Biomedical Research  
University of Victoria  
PO Box 3020 STN CSC, Victoria BC, V8W 3N5, Canada  
Tel: 250 472 4067  
Fax: 250 472 4075  
Email: bkoop@uvic.ca  
Centre for Biomedical Research, University of Victoria cDNA  
preparation and sequencing: Roberto Alberto, Marianne  
Beetz-Sargent, Maura Busby, Peter Hunt, Linda McKinnel, BF Koop.  
bioinformatics: Gordon D Brown.

**FEATURES**  
source  
1. .433  
/organism="Oncorhynchus mykiss"  
/mol\_type="mRNA"  
/strain="Chilliack River steelhead"  
/db\_xref="taxon:8022"  
/clone\_lib="Oncorhynchus mykiss Chilliack River steelhead  
whole"  
/note="Vector: pBlueScriptIISK+; Library Creator: Matthew  
L Rise, BF Koop; Rainbow trout tissue contributors:  
Robert Devlin (DFO, Vancouver, B.C.)"

**ORIGIN**  
Query Match 72.7%; Score 16; DB 14; Length 433;  
Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CACTGGTCTTCTGTG 21  
|||||  
Db 238 CACTGGTCTTCTGTG 223  
|||||

**RESULT 11**  
CB495414  
LOCUS  
DEFINITION Omykswel006021 Oncorhynchus mykiss Chilliack River steelhead whole  
Oncorhynchus mykiss cDNA, mRNA sequence.  
ACCESSION  
VERSION CB495414.1 GI:29306640  
KEYWORDS  
SOURCE  
ORGANISM  
Oncorhynchus mykiss (rainbow trout)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
REFERENCE  
1 (bases 1 to 433)  
AUTHORS GRASP Consortium, Davidson, W.S., Koop, B.F. and  
http://web.uvic.ca/chr/grasp.  
TITLE A survey of Salmo salar transcripts from high complexity cDNA  
libraries  
JOURNAL  
COMMENT Unpublished (2002)  
Contact: Koop BF  
Centre for Biomedical Research  
University of Victoria  
PO Box 3020 STN CSC, Victoria BC, V8W 3N5, Canada  
Tel: 250 472 4067  
Fax: 250 472 4075  
Email: bkoop@uvic.ca  
Centre for Biomedical Research, University of Victoria cDNA  
preparation and sequencing: Roberto Alberto, Marianne  
Beetz-Sargent, Maura Busby, Peter Hunt, Linda McKinnel, BF Koop.  
bioinformatics: Gordon D Brown.

**FEATURES**  
source  
1. .433  
/organism="Oncorhynchus mykiss"  
/mol\_type="mRNA"  
/strain="Chilliack River steelhead"  
/db\_xref="taxon:8022"  
/clone\_lib="Oncorhynchus mykiss Chilliack River steelhead  
whole"  
/note="Vector: pBlueScriptIISK+; Library Creator: Matthew  
L Rise, BF Koop; Rainbow trout tissue contributors:  
Robert Devlin (DFO, Vancouver, B.C.)"

**ORIGIN**  
Query Match 72.7%; Score 16; DB 14; Length 433;  
Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CACTGGTCTTCTGTG 21  
|||||  
Db 196 CACTGGTCTTCTGTG 211  
|||||

**RESULT 12**  
CB495567  
LOCUS  
DEFINITION Omykswel006066 Oncorhynchus mykiss Chilliack River steelhead whole  
Oncorhynchus mykiss cDNA, mRNA sequence.  
ACCESSION  
VERSION CB495567  
KEYWORDS  
SOURCE  
ORGANISM  
Oncorhynchus mykiss (rainbow trout)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
REFERENCE  
1 (bases 1 to 433)  
AUTHORS GRASP Consortium, Davidson, W.S., Koop, B.F. and  
http://web.uvic.ca/chr/grasp.  
TITLE A survey of Salmo salar transcripts from high complexity cDNA  
libraries  
JOURNAL  
COMMENT Unpublished (2002)  
Contact: Koop BF  
Centre for Biomedical Research  
University of Victoria  
PO Box 3020 STN CSC, Victoria BC, V8W 3N5, Canada  
Tel: 250 472 4067  
Fax: 250 472 4075  
Email: bkoop@uvic.ca  
Centre for Biomedical Research, University of Victoria cDNA  
preparation and sequencing: Roberto Alberto, Marianne  
Beetz-Sargent, Maura Busby, Peter Hunt, Linda McKinnel, BF Koop.  
bioinformatics: Gordon D Brown.

**FEATURES**  
source  
1. .433  
/organism="Oncorhynchus mykiss"  
/mol\_type="mRNA"  
/strain="Chilliack River steelhead"  
/db\_xref="taxon:8022"  
/clone\_lib="Oncorhynchus mykiss Chilliack River steelhead  
whole"  
/note="Vector: pBlueScriptIISK+; Library Creator: Matthew  
L Rise, BF Koop; Rainbow trout tissue contributors:  
Robert Devlin (DFO, Vancouver, B.C.)"

**ORIGIN**  
Query Match 72.7%; Score 16; DB 14; Length 433;  
Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CACTGGTCTTCTGTG 21  
|||||  
Db 196 CACTGGTCTTCTGTG 211  
|||||

**RESULT 13**  
BY505647/c  
LOCUS  
DEFINITION RIKEN full-length enriched, bone marrow macrophage Mus  
musculus cDNA clone I830091A16 3', mRNA sequence.  
ACCESSION  
VERSION BY505647.1 GI:26840026  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)  
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 451)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaide, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojohori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V., Chothia, C., Corbani, L. E., Cousins, S., Dalia, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Karai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Perte, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

22354683

12466951

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsc.riken.go.jp/

URL: <http://genome.gsc.riken.go.jp/>

Aizawa, K., Akimura, T., Arakawa, I., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission

Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by David A. Hume ( Depts. of Biochemistry and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane, Q 4072 Australia ) whose assistance we gratefully acknowledge.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

Location/Qualifiers

source

1. .451

/organism="Mus musculus"

/mol\_type="mRNA"

/strains="CS7BL/6J"

/db\_xref="taxon:10090"

/clone="I830091A16"

/tissue\_type="bone marrow"

/cell\_type="macrophage"

/clone\_lib="RIKEN full-length enriched, bone marrow macrophage"

ORIGIN

Query Match 72.7%; Score 16; DB 13; Length 451;

Best Local Similarity 100.0%; Pred. No. 6.8e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ACCACTGGTCTCTTG 19

|||||

Db 351 ACCACTGGTCTCTTG 336

RESULT 14

LOCUS BF388753 456 bp mRNA linear EST 27-NOV-2000

DEFINITION UI-R-BS2-bde-b-08-0-UI.s1 UI-R-BS2 Rattus norvegicus cDNA clone

ACCESSION BF388753

VERSION BF388753.1 GI:11373577

KEYWORDS EST.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

REFERENCE 1 (bases 1 to 456)

AUTHORS Ronaldo, M.F., Lennon, G. and Soares, M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477

PUBMED 889548

COMMENT Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road, 4156 MEBRP, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

The sequence contained an oligo-dT track that was present in the strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the normalized embryo at 13 dpc library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics ([www.resgen.com](http://www.resgen.com))

Seq primer: M13 Forward

POLYA=Yes.

Location/Qualifiers

1. .456

/organism="Rattus norvegicus"

/mol\_type="mRNA"

/strains="Sprague-Dawley"

/db\_xref="taxon:10116"

/clone="UI-R-BS2-bde-b-08-0-UI"

/dev\_stage="embryonic 13 dpc"

/lab\_host="DHI0B (Life Technologies)"

/clone\_lib="UI-R-BS2"

/notes="Vector: p773D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-BS2 library is a subtracted library derived from 13 dpc whole embryo tissue. For a detailed description of the library from which this clone was derived, please visit our web

FEATURES

source

site at ratseq.eng.uiowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)  
TAG\_TISSUE=embryo at 13 dpc  
TAG\_LIB=UI-R-BS2  
TAG\_SEQ=AATCC"

## ORIGIN

Query Match 72.7%; Score 16; DB 10; Length 456;  
Best Local Similarity 100.0%; Pred. No. 6.8e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 CACTGGTCTTCTTG 21  
|||||  
DB 129 CACTGGTCTTCTTG 114

## RESULT 15

BF402543/c 500 bp mRNA linear EST 28-NOV-2000  
LOCUS  
DEFINITION  
UI-R-CA0-bhr-f-05-0-UI.s1 UI-R-CA0 Rattus norvegicus cDNA clone  
UI-R-CA0-bhr-f-05-0-UI 3', mRNA sequence.

ACCESSION  
BF402543

VERSION  
BF402543.1 GI:11390518

KEYWORDS  
EST.

SOURCE  
Rattus norvegicus (Norway rat)

ORGANISM  
Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

REFERENCE  
1 (bases 1 to 500)

AUTHORS  
Bonaldo, M.F., Lennon, G. and Soares, M.B.

TITLE  
Normalization and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

JOURNAL  
MEDLINE  
97044477

PUBMED  
8889548

## COMMENT

Contact: Soares, MB  
Coordinated Laboratory for Computational Genomics  
University of Iowa  
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: bento-soares@uiowa.edu

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA library preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com)  
Seq primer: M13 Forward  
POLYA=Yes.

## FEATURES

Location/Qualifiers

1..500  
/organism="Rattus norvegicus"  
/mol\_type="mRNA"  
/strain="Sprague-Dawley"  
/db\_xref="taxon:10116"  
/clone="UI-R-CA0-bhr-f-05-0-UI"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="UI-R-CA0"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not 1; Site\_2: Eco RI; The UI-R-CA0 library is a subtracted library derived from the following tissues: thalamus, cerebellum, hypothalamus, medulla, pons, midbrain, cerebral cortex, corpus striatum, testis, and hippocampus. For a detailed description of the library from which this clone was derived, please visit our web site at ratseq.eng.uiowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)  
TAG\_SEQ=None found"

## ORIGIN

Query Match 72.7%; Score 16; DB 10; Length 500;  
Best Local Similarity 100.0%; Pred. No. 6.8e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 CACTGGTCTTCTTG 21  
|||||  
DB 129 CACTGGTCTTCTTG 114

Search completed: August 2, 2004, 20:28:01

Job time : 912.207 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 2, 2004, 18:10:40 ; Search time 22.1897 Seconds  
(without alignments)  
550.208 Million cell updates/sec

Title: US-10-068-067-18  
Perfect score: 22  
Sequence: 1 cttgtgtttatccgggcaagaa 22

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents, NA.\*  
1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/2/ina/PTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/2/ina/backfiles.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	21	95.5	1193	4	US-08-720-565-3
2	14	63.6	1262	4	US-09-212-609B-29
3	14	63.6	1262	4	US-09-064-411A-31
4	14	63.6	1267	4	US-09-064-411A-22
5	14	63.6	1267	4	US-09-280-428A-9
6	14	63.6	1456	4	US-09-064-411A-23
7	14	63.6	1578	4	US-09-252-991A-5039
8	14	63.6	1581	4	US-09-252-991A-5177
9	13	59.1	24	3	US-08-943-731-498
10	13	59.1	511	3	US-08-943-731-441
11	13	59.1	905	4	US-09-221-017B-560
12	13	59.1	948	4	US-09-134-001C-949
13	13	59.1	987	4	US-09-543-681A-323
14	13	59.1	1197	4	US-09-489-039A-2370
15	13	59.1	3762	3	US-09-318-448-17
16	13	59.1	2183	3	US-08-943-731-3
17	13	59.1	3524	3	US-08-923-137-1
18	13	59.1	4484	4	US-09-435-739-42
19	13	59.1	72928	3	US-09-009-913-1
20	13	59.1	1830121	4	US-09-557-884-1
21	13	59.1	1830121	4	US-09-643-990A-1
22	12	54.5	99	3	US-08-995-156A-10
23	12	54.5	99	4	US-09-419-281-10
24	12	54.5	281	4	US-08-469-260A-18
25	12	54.5	281	4	US-08-469-260A-20
26	12	54.5	281	4	US-08-488-446-18
27	12	54.5	281	4	US-08-488-446-20

28	12	54.5	281	4	US-08-467-344A-18	Sequence 18, Appl
29	12	54.5	281	4	US-08-467-344A-20	Sequence 20, Appl
30	12	54.5	282	4	US-08-150-204B-114	Sequence 114, Appl
31	12	54.5	285	3	US-08-995-156A-6	Sequence 6, Appl
32	12	54.5	285	4	US-09-419-281-6	Sequence 6, Appl
33	12	54.5	293	4	US-09-313-294A-3746	Sequence 3746, Ap
34	12	54.5	329	4	US-09-702-705-409	Sequence 409, Ap
35	12	54.5	329	4	US-09-736-457-409	Sequence 409, Ap
36	12	54.5	329	4	US-09-614-124B-409	Sequence 409, Ap
37	12	54.5	329	4	US-09-671-325-409	Sequence 409, Ap
38	12	54.5	329	4	US-09-589-184-409	Sequence 409, Ap
39	12	54.5	351	4	US-09-252-991A-2525	Sequence 2525, Ap
40	12	54.5	396	4	US-09-640-173-161	Sequence 161, Ap
41	12	54.5	396	4	US-09-713-550-161	Sequence 161, Ap
42	12	54.5	403	4	US-09-621-976-11017	Sequence 11017, A
43	12	54.5	414	4	US-09-489-039A-4044	Sequence 4044, Ap
44	12	54.5	432	4	US-09-252-991A-14394	Sequence 14394, A
45	12	54.5	459	4	US-09-543-681A-681	Sequence 681, Ap

ALIGNMENTS

RESULT 1  
US-08-720-565-3  
Sequence 3, Application US/08720565  
Patent No. 6537764  
GENERAL INFORMATION:  
APPLICANT: Gerard, Craig J.  
APPLICANT: Gerard, No. 6537764ma P.  
APPLICANT: Mackay, Charles R.  
APPLICANT: Ponath, Paul D.  
APPLICANT: Post, Theodore W.  
APPLICANT: Qin, Shixin  
TITLE OF INVENTION: G PROTEIN-COUPLED RECEPTOR GENE CCR3 AND  
TITLE OF INVENTION: ANTAGONISTS THEREOF  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02173

COMPUTER READABLE FORM: disk  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/720,565  
FILING DATE: 30-SEP-1996  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/00608  
FILING DATE: 19-JAN-1996  
PRIOR APPLICATION DATA: US 08/375,199  
FILING DATE: 19-JAN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Brook, David E.  
REGISTRATION NUMBER: 22,592  
REFERENCE/DOCKET NUMBER: LKS94-05A2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1193 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA



ATTORNEY/AGENT INFORMATION:  
NAME: Borucki, Andrea T.  
REGISTRATION NUMBER: 33651  
REFERENCE/DOCKET NUMBER: 50433  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 317-337-4846  
TELEFAX: 317-337-4847  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1267 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-09-064-411A-22

Query Match 63.6%; Score 14; DB 4; Length 1267;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTGCTTATCCGGC 17  
|||||  
DB 1074 GTGCTTATCCGGC 1061

RESULT 5  
US-09-280-428A-9/c  
Sequence 9, Application US/09280428A  
Patent No. 6495738  
GENERAL INFORMATION:  
APPLICANT: Folkerts, Otto  
APPLICANT: Merlo, Donald J  
TITLE OF INVENTION: Modification of Fatty Acid Composition in Plants by  
TITLE OF INVENTION: Expression of A Fungal Acyl-CoA Desaturase  
FILE REFERENCE: 50612  
CURRENT APPLICATION NUMBER: US/09/280,428A  
CURRENT FILING DATE: 1999-03-29  
PRIOR APPLICATION NUMBER: 60/079840  
PRIOR FILING DATE: 1998-03-30  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 9  
LENGTH: 1267  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: portion of  
OTHER INFORMATION: ppgn62-2  
US-09-280-428A-9

Query Match 63.6%; Score 14; DB 4; Length 1267;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTGCTTATCCGGC 17  
|||||  
DB 1074 GTGCTTATCCGGC 1061

RESULT 6  
US-09-064-411A-23/c  
Sequence 23, Application US/09064411A  
Patent No. 6331664  
GENERAL INFORMATION:  
APPLICANT: Rubin-Wilson, Beth  
APPLICANT: Guo, Lining  
APPLICANT: Skokut, Tom  
APPLICANT: Young, Scott  
APPLICANT: Folkerts, Otto  
APPLICANT: Armstrong, Katherine  
APPLICANT: Cowen, Neil M.  
TITLE OF INVENTION: Nucleotide Sequences of Maize Oleoyl-ACP  
TITLE OF INVENTION: Thioesterase and Palmitoyl-ACP Thioesterase Genes and

TITLE OF INVENTION: Their Use In The Regulation of Fatty Acid Content of Oil  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Dow AgroSciences Patent Department  
STREET: 9330 Zionsville Road  
CITY: Indianapolis  
STATE: Indiana  
COUNTRY: USA  
ZIP: 46268  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/064,411A  
FILING DATE: 22-APR-1998  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/045,827  
FILING DATE: 05-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Borucki, Andrea T.  
REGISTRATION NUMBER: 33651  
REFERENCE/DOCKET NUMBER: 50433  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 317-337-4846  
TELEFAX: 317-337-4847  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1456 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-09-064-411A-23

Query Match 63.6%; Score 14; DB 4; Length 1456;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTGCTTATCCGGC 17  
|||||  
DB 1265 GTGCTTATCCGGC 1252

RESULT 7  
US-09-252-991A-5039/c  
Sequence 5039, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 5039  
LENGTH: 1578  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-5039

Query Match 63.8%; Score 14; DB 4; Length 1578;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CTTATCCGGCAAG 20

Db 425 CTTATCGGCGAAG 412  
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RESULT 8  
US-09-252-991A-5177  
; Sequence 5177, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 5177  
; LENGTH: 1581  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-5177  
Query Match 63.6%; Score 14; DB 4; Length 1581;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 CTTATCGGCGAAG 20  
|||||  
Db 1247 CTTATCGGCGAAG 1260  
|||||  
RESULT 9  
US-08-943-731-498  
; Sequence 498, Application US/08943731  
; Patent No. 6265157  
; GENERAL INFORMATION:  
; APPLICANT: PROCKOP, DARWIN J.  
; APPLICANT: SPOTILA, LORETTA D.  
; APPLICANT: DELTAS, CONSTANTINOS D.  
; APPLICANT: SEREDA, LARISA  
; APPLICANT: LARSON, ANDREA W.  
; APPLICANT: PACK, MICHAEL  
; APPLICANT: COLIGE, ALAIN  
; APPLICANT: EARLY, JAMES  
; APPLICANT: KORKKO, JARMO  
; APPLICANT: ALA-KOKKO, LEENA, et al.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING  
; TITLE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES  
; NUMBER OF SEQUENCES: 666  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.  
; STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND  
; STREET: FLR.  
; CITY: PHILADELPHIA  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19103-7086  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/943,731  
; FILING DATE: 03-OCT-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/212,322  
; FILING DATE: 14-MAR-1994

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/803,628  
; FILING DATE: 03-DEC-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DOYLE LEARY Ph.D., KATHRYN  
; REGISTRATION NUMBER: 36,317  
; REFERENCE/DOCKET NUMBER: 9598-27  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-365-1284  
; TELEFAX: 215-567-2991  
; TELEX: 831-494  
; INFORMATION FOR SEQ ID NO: 498:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 24 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-943-731-498  
Query Match 59.1%; Score 13; DB 3; Length 24;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTTGTGCTTATCC 13  
|||||  
Db 12 CTTGTGCTTATCC 24  
|||||  
RESULT 10  
US-08-943-731-141  
; Sequence 141, Application US/08943731  
; Patent No. 6265157  
; GENERAL INFORMATION:  
; APPLICANT: PROCKOP, DARWIN J.  
; APPLICANT: SPOTILA, LORETTA D.  
; APPLICANT: DELTAS, CONSTANTINOS D.  
; APPLICANT: SEREDA, LARISA  
; APPLICANT: LARSON, ANDREA W.  
; APPLICANT: PACK, MICHAEL  
; APPLICANT: COLIGE, ALAIN  
; APPLICANT: EARLY, JAMES  
; APPLICANT: KORKKO, JARMO  
; APPLICANT: ALA-KOKKO, LEENA, et al.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING  
; TITLE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES  
; NUMBER OF SEQUENCES: 666  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.  
; STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND  
; STREET: FLR.  
; CITY: PHILADELPHIA  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19103-7086  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/943,731  
; FILING DATE: 03-OCT-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/212,322  
; FILING DATE: 14-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/803,628  
; FILING DATE: 03-DEC-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DOYLE LEARY Ph.D., KATHRYN  
; REGISTRATION NUMBER: 36,317



; REFERENCE/DOCKET NUMBER: 9598-27  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-965-1284  
; TELEFAX: 215-567-2991  
; TELEX: 831-494  
; INFORMATION FOR SEQ ID NO: 141:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 511 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-943-731-141

Query Match 59.1%; Score 13; DB 3; Length 511;  
Best Local Similarity 100.0%; Pred. No. 51;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTGTGCTTATCC 13  
Db 421 CTTGTGCTTATCC 433

## RESULT 11

US-09-221-017B-560/c  
; Sequence 560, Application US/09221017B  
; Patent No. 6444799  
; GENERAL INFORMATION:

; APPLICANT: Ross, Bruce C.  
; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF  
; NUMBER OF SEQUENCES: 1120  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018

## COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/221,017B  
; FILING DATE: 23-DEC-1998  
; CLASSIFICATION:

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PP1182  
; FILING DATE: 31-DEC-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PP1546  
; FILING DATE: 30-JAN-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PP2911  
; FILING DATE: 09-APR-1998

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/AU98/01023  
; FILING DATE: 10-DEC-1998

; ATTORNEY/AGENT INFORMATION:  
; NAME: Monroy, Gladys H

; REGISTRATION NUMBER: 32,430  
; REFERENCE/DOCKET NUMBER: 27340-20021.00  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-813-5600  
; TELEFAX: 650-494-0792  
; TELEX: 706141

; INFORMATION FOR SEQ ID NO: 560:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 905 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: circular

; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: UNKNOWN  
; ORIGINAL SOURCE:  
; ORGANISM: PORYPHYROMONAS GINGIVALIS  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 1...905  
US-09-221-017B-560

Query Match 59.1%; Score 13; DB 4; Length 905;  
Best Local Similarity 100.0%; Pred. No. 51;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 TATCCGGGCAAGA 21  
Db 547 TATCCGGGCAAGA 535

## RESULT 12

US-09-134-001C-949  
; Sequence 949, Application US/09134001C  
; Patent No. 6380370  
; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC-007

; CURRENT APPLICATION NUMBER: US/09/134,001C  
; CURRENT FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08

; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14

; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 949  
; TYPE: DNA

; LENGTH: 948

; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-949

Query Match 59.1%; Score 13; DB 4; Length 948;  
Best Local Similarity 100.0%; Pred. No. 51;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GTGCTTATCCGGG 16  
Db 476 GTGCTTATCCGGG 488

## RESULT 13

US-09-543-681A-323  
; Sequence 323, Application US/09543681A  
; Patent No. 6605709  
; GENERAL INFORMATION:

; APPLICANT: GARY BRETON  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS

; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.1002-001

; CURRENT APPLICATION NUMBER: US/09/543,681A  
; CURRENT FILING DATE: 2000-04-05

; PRIOR APPLICATION NUMBER: US 60/128,706  
; PRIOR FILING DATE: 1999-04-09

; NUMBER OF SEQ ID NOS: 8344  
; SEQ ID NO 323  
; LENGTH: 987

; TYPE: DNA

; ORGANISM: Proteus mirabilis  
US-09-543-681A-323

Query Match 59.1%; Score 13; DB 4; Length 987;  
Best Local Similarity 100.0%; Pred. No. 51;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTGCTTATCCGGG 16  
| | | | | | | | | |  
Db 521 GTGCTTATCCGGG 533

## RESULT 14

US-09-489-039A-2370  
; Sequence 2370, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 2370  
; LENGTH: 1197  
; TYPE: DNA  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-2370

Query Match 59.1%; Score 13; DB 4; Length 1197;  
Best Local Similarity 100.0%; Pred. No. 51;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GCTTATCCGGGCA 18  
| | | | | | | | | |  
Db 321 GCTTATCCGGGCA 333

## RESULT 15

US-09-318-448-17/c  
; Sequence 17, Application US/09318448  
; Patent No. 6210950  
; GENERAL INFORMATION:  
; APPLICANT: Johnson, William G.  
; APPLICANT: Stenroos, Edward S.  
; TITLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, AND TREATING  
; TITLE OF INVENTION: DEVELOPMENTAL DISORDERS  
; FILE REFERENCE: 601-1-057  
; CURRENT APPLICATION NUMBER: US/09/318,448  
; CURRENT FILING DATE: 1999-05-25  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 17  
; LENGTH: 3762  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-318-448-17

Query Match 59.1%; Score 13; DB 3; Length 3762;  
Best Local Similarity 100.0%; Pred. No. 51;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGTGCTTATCC 13  
| | | | | | | | | |  
Db 2217 CTTGTGCTTATCC 2205

Search completed: August 2, 2004, 20:30:05  
Job time : 24.1897 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 2, 2004, 16:56:38 ; Search time 106.207 Seconds  
(without alignments)  
879.984 Million cell updates/sec

Title: US-10-068-067-18

Perfect score: 22

Sequence: 1 cttgtcctatccgggcaagaa 22

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 337863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N Geneseq\_29Jan04.\*

1: geneseqn1980s.\*

2: geneseqn1990s.\*

3: geneseqn2000s.\*

4: geneseqn2001as.\*

5: geneseqn2001bs.\*

6: geneseqn2002s.\*

7: geneseqn2003as.\*

8: geneseqn2003bs.\*

9: geneseqn2003cs.\*

10: geneseqn2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	100.0	22	ABQ78516	ABQ78516 Nucleotid
2	22	100.0	22	ABQ78521	ABQ78521 Nucleotid
3	22	100.0	51	ABQ78514	ABQ78514 Nucleotid
4	22	100.0	51	ABQ78519	ABQ78519 Nucleotid
5	22	100.0	2895	ABQ78513	ABQ78513 Nucleotid
6	21	95.5	1193	AAT31335	AAT31335 CC-Chemok
7	21	95.5	1193	AAV07403	AAV07403 Human C-C
8	16	72.7	265	ABX50975	ABX50975 Bovine ES
9	15	68.2	23654	AB117664	AB117664 Drosophila
10	14	63.6	438	AB12176	AB12176 Alloioococ
11	14	63.6	717	ABK75795	ABK75795 Bacillus
12	14	63.6	945	AAK91767	AAK91767 Porphyrom
13	14	63.6	987	AAK91633	AAK91633 Porphyrom
14	14	63.6	1262	AAV80227	AAV80227 Maize glo
15	14	63.6	1262	ABA94959	ABA94959 Globulin
16	14	63.6	1267	AAV80218	AAV80218 Maize glo
17	14	63.6	1267	AAK90960	AAK90960 Nucleotid
18	14	63.6	1432	AAK57151	AAK57151 Maize glo
19	14	63.6	1456	AAV80219	AAV80219 Maize glo
20	14	63.6	2235	ADD48617	ADD48617 Rat gene
21	14	63.6	2331	AD12180	AD12180 Alloioococ
22	14	63.6	2331	AB12178	AB12178 Alloioococ
23	14	63.6	3017	AAK86511	AAK86511 DNA const

24	14	63.6	3408	7	ABT17984	Abt17984 Aspergill
25	14	63.6	3409	7	ABT17998	Abt17998 Aspergill
26	14	63.6	5511	2	AZ08718	Az08718 Chimeric
27	14	63.6	54382	8	ADB12064_17	Continuation (18 o
28	13	59.1	24	5	AAS22266	Aas22266 Human COL
29	13	59.1	193	6	ABN73948	Abn73948 Bovine em
30	13	59.1	215	4	AAK79563	Aak79563 Human imm
31	13	59.1	228	5	AAS69713	Aas69713 DNA encod
32	13	59.1	260	6	ABL79816	Ab179816 Human ova
33	13	59.1	375	7	ACA43197	Aca43197 Prokaryot
34	13	59.1	411	6	ABN70758	Abn70758 Streptoco
35	13	59.1	420	6	ABK78358	Abk78358 Bacillus
36	13	59.1	425	8	ACH40149	Ach40149 Human foe
37	13	59.1	492	6	ABN26019	Abn26019 Human ORF
38	13	59.1	493	9	ADE81829	Ade81829 Arabidops
39	13	59.1	511	5	AAS21909	Aas21909 Human col
40	13	59.1	537	3	AAC36765	Aac36765 Arabidops
41	13	59.1	539	4	AAS58713	Aas58713 cDNA #138
42	13	59.1	566	8	ACH39350	Ach39350 Human foe
43	13	59.1	671	6	ABK29826	Abk29826 Colon ade
44	13	59.1	690	6	AAL48404	Aal48404 Human ser
45	13	59.1	690	6	AAD34463	Aad34463 Human ser

## ALIGNMENTS

### RESULT 1

ABQ78516

ID ABQ78516 standard; DNA; 22 BP.

XX AC

XX ABQ78516;

XX AC

DT 25-NOV-2002 (first entry)

XX DE

XX Nucleotide sequence of a regulatory sequence for human CCR3.

XX Human, CC chemokine receptor 3; CCR3; allergic disorder; probe;

KW inflammatory disorder; eosinophil; hypersensitivity; leukemia;

KW infectious disorder; HIV; respiratory syncytial virus infection; ss.

XX OS

XX Homo sapiens.

XX PN

XX WC200262848-A2.

XX PD

XX 15-AUG-2002.

XX PF

XX 06-FEB-2002; 2002WO-US003442.

XX PR

XX 07-FEB-2001; 2001US-0267073P.

XX PR

XX 05-FEB-2002; 2002US-00068067.

XX PA

XX (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.

XX PI

XX Rothenberg ME, Zimmerman N;

XX DR

XX WPI; 2002-657524/70.

XX PT

XX New CC chemokine receptor 3 (CCR3) regulatory site in an untranslated

PT exon 1, exon 2, exon 3 or promoter of a human CCR3 gene or mRNA capable

FT of binding to regulatory elements, useful for preventing e.g. allergic

FT inflammatory reactions.

XX PS

XX Claim 6; Page 54; 56pp; English.

XX CC

XX The present sequence represents a probe for the human CC chemokine

CC receptor 3 (CCR3) gene. The probe is a regulatory sequence for CCR3. CCR3

CC is expressed on cells involved in allergic and/or inflammatory disorders.

CC The gene comprises 4 exons, with the coding region present on exon 4. The

CC specification describes methods of regulating the expression of CCR3. The

CC regulatory site is derived from an untranslated exon 1, exon 2, exon 3 or

CC promoter of a human CCR3 gene. Regulating the expression of the chemokine

CC receptor CCR3 is useful for preventing or treating disorders involving

CC eosinophils, such as allergic inflammatory and hypersensitivity  
 CC reactions, certain types of leukemia, and certain infectious disorders  
 CC involving CCR3, e.g. HIV or respiratory syncytial virus infection.  
 CC Expression and modulation of CCR3 is a useful tool in assessing  
 CC eosinophil targeting and in regulating eosinophil-mediated reactions and  
 CC diseases  
 XX  
 SQ Sequence 22 BP; 5 A; 5 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 6; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 0.0016;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGTGCTTATCCGGCAAGAA 22  
 |||||  
 Db 1 CTTGTGCTTATCCGGCAAGAA 22

## RESULT 2

ABQ78521  
 ID ABQ78521 standard; RNA; 22 BP.

AC ABQ78521;

DT 25-NOV-2002 (first entry)

DE Nucleotide sequence of a regulatory sequence for human CCR3.

KW Human; CC chemokine receptor 3; CCR3; allergic disorder; probe;  
 KW inflammatory disorder; eosinophil; hypersensitivity; leukemia;  
 KW infectious disorder; HIV; respiratory syncytial virus infection; ss.

OS Homo sapiens.

PN WO200262848-A2.

PD 15-AUG-2002.

PF 06-FEB-2002; 2002WO-US003442.

PR 07-FEB-2001; 2001US-0267073P.

PR 05-FEB-2002; 2002US-00068067.

PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.

PI Rothenberg ME, Zimmermann N;

PS WPI; 2002-657524/70.

PT New CC chemokine receptor 3 (CCR3) regulatory site in an untranslated  
 PT exon 1, exon 2, exon 3 or promoter of a human CCR3 gene or mRNA capable  
 PT of binding to regulatory elements, useful for preventing e.g. allergic  
 PT inflammatory reactions.

PS Claim 8; Page 56; 56pp; English.

XX The present sequence represents a probe for the human CC chemokine  
 XX receptor 3 (CCR3) gene. The probe is a regulatory sequence for CCR3. CCR3  
 XX is expressed on cells involved in allergic and/or inflammatory disorders.  
 XX The gene comprises 4 exons, with the coding region present on exon 4. The  
 XX specification describes methods of regulating the expression of CCR3. The  
 XX regulatory site is derived from an untranslated exon 1, exon 2, exon 3 or  
 XX promoter of a human CCR3 gene. Regulating the expression of the chemokine  
 XX receptor CCR3 is useful for preventing or treating disorders involving  
 XX eosinophils, such as allergic inflammatory and hypersensitivity  
 XX reactions, certain types of leukemia, and certain infectious disorders  
 XX involving CCR3, e.g. HIV or respiratory syncytial virus infection.  
 XX Expression and modulation of CCR3 is a useful tool in assessing  
 XX eosinophil targeting and in regulating eosinophil-mediated reactions and  
 XX diseases

SQ Sequence 22 BP; 5 A; 5 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 6; Length 22;  
 Best Local Similarity 72.7%; Pred. No. 0.0016;  
 Matches 16; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGTGCTTATCCGGCAAGAA 22  
 |||||  
 Db 1 CUUGUGCUUAUCCGGCAAGAA 22

## RESULT 3

ABQ78514  
 ID ABQ78514 standard; DNA; 51 BP.

XX AC ABQ78514;

DT 25-NOV-2002 (first entry)

DE Nucleotide sequence of a regulatory sequence for human CCR3.

KW Human; CC chemokine receptor 3; CCR3; allergic disorder; probe;  
 KW inflammatory disorder; eosinophil; hypersensitivity; leukemia;  
 KW infectious disorder; HIV; respiratory syncytial virus infection; ss.

OS Homo sapiens.

PN WO200262848-A2.

PD 15-AUG-2002.

PF 06-FEB-2002; 2002WO-US003442.

PR 07-FEB-2001; 2001US-0267073P.

PR 05-FEB-2002; 2002US-00068067.

PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.

PI Rothenberg ME, Zimmermann N;

PS WPI; 2002-657524/70.

PT New CC chemokine receptor 3 (CCR3) regulatory site in an untranslated  
 PT exon 1, exon 2, exon 3 or promoter of a human CCR3 gene or mRNA capable  
 PT of binding to regulatory elements, useful for preventing e.g. allergic  
 PT inflammatory reactions.

PS Claim 2; Page 25; 56pp; English.

XX The present sequence represents a probe for the human CC chemokine  
 XX receptor 3 (CCR3) gene. The probe comprises +10 to +60 of exon 1 of CCR3,  
 XX and is a regulatory sequence for CCR3. CCR3 is expressed on cells  
 XX involved in allergic and/or inflammatory disorders. The gene comprises 4  
 XX exons, with the coding region present on exon 4. The specification  
 XX describes methods of regulating the expression of CCR3. The regulatory  
 XX site is derived from an untranslated exon 1, exon 2, exon 3 or promoter  
 XX of a human CCR3 gene. Regulating the expression of the chemokine receptor  
 XX CCR3 is useful for preventing or treating disorders involving  
 XX eosinophils, such as allergic inflammatory and hypersensitivity  
 XX reactions, certain types of leukemia, and certain infectious disorders  
 XX involving CCR3, e.g. HIV or respiratory syncytial virus infection.  
 XX Expression and modulation of CCR3 is a useful tool in assessing  
 XX eosinophil targeting and in regulating eosinophil-mediated reactions and  
 XX diseases

SQ Sequence 51 BP; 13 A; 12 C; 11 G; 15 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 6; Length 51;  
 Best Local Similarity 100.0%; Pred. No. 0.0016;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGTGCTTATCCGGCAAGAA 22  
 DB 16 CTTGTGCTTATCCGGCAAGAA 37

RESULT 4  
 ABQ78519  
 ID ABQ78519 standard; RNA; 51 BP.  
 XX AC ABQ78519;  
 XX DT 25-NOV-2002 (first entry)  
 XX DE Nucleotide sequence of a regulatory sequence for human CCR3.  
 XX KW Human; CC chemokine receptor 3; CCR3; allergic disorder; probe;  
 XX KW inflammatory disorder; eosinophil; hypersensitivity; leukemia;  
 XX KW infectious disorder; HIV; respiratory syncytial virus infection; ss.  
 XX OS Homo sapiens.  
 XX FN WO200262848-A2.  
 XX PD 15-AUG-2002.  
 XX PF 06-FEB-2002; 2002WO-US003442.  
 XX PR 07-FEB-2001; 2001US-0267073P.  
 XX PR 05-FEB-2002; 2002US-00068067.  
 XX PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
 XX PI Rothenberg ME, Zimmerman N;  
 XX DR WPI; 2002-657524/70.  
 XX PT New CC chemokine receptor 3 (CCR3) regulatory site in an untranslated  
 exon 1, exon 2, exon 3 or promoter of a human CCR3 gene or mRNA capable  
 of binding to regulatory elements, useful for preventing e.g. allergic  
 inflammatory reactions.  
 XX PS Claim 7; Page 56; 56pp; English.

The present sequence represents a probe for the human CC chemokine  
 receptor 3 (CCR3) gene. The probe is a regulatory sequence for CCR3. CCR3  
 is expressed on cells involved in allergic and/or inflammatory disorders.  
 The gene comprises 4 exons, with the coding region present on exon 4. The  
 specification describes methods of regulating the expression of CCR3. The  
 regulatory site is derived from an untranslated exon 1, exon 2, exon 3 or  
 promoter of a human CCR3 gene. Regulating the expression of the chemokine  
 receptor CCR3 is useful for preventing or treating disorders involving  
 eosinophils, such as allergic inflammatory and hypersensitivity  
 reactions, certain types of leukemia, and certain infectious disorders  
 involving CCR3, e.g. HIV or respiratory syncytial virus infection.  
 Expression and modulation of CCR3 is a useful tool in assessing  
 eosinophil targeting and in regulating eosinophil-mediated reactions and  
 diseases

Sequence 51 BP; 13 A; 12 C; 11 G; 0 T; 15 U; 0 Other;

Query Match 100.0%; Score 22; DB 6; Length 51;  
 Best Local Similarity 72.7%; Pred. No. 0.0016;  
 Matches 16; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGTGCTTATCCGGCAAGAA 22  
 DB 16 CUUGGCUUACCGGCAAGAA 37

RESULT 5  
 ABQ78513  
 ID ABQ78513 standard; DNA; 2895 BP.  
 XX AC ABQ78513;  
 XX DT 25-NOV-2002 (first entry)  
 XX DE Nucleotide sequence of the human CCR3 gene promoter.  
 XX KW Human; CC chemokine receptor 3; CCR3; allergic disorder;  
 XX KW inflammatory disorder; eosinophil; hypersensitivity; leukemia;  
 XX KW infectious disorder; HIV; respiratory syncytial virus infection;  
 XX KW promoter; ss.  
 XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 FT misc\_signal 1640..1645  
 FT /\*tag= a  
 FT /note= "splice donor consensus site"  
 XX PN WO200262848-A2.  
 XX PD 15-AUG-2002.  
 XX PF 06-FEB-2002; 2002WO-US003442.  
 XX PR 07-FEB-2001; 2001US-0267073P.  
 XX PR 05-FEB-2002; 2002US-00068067.  
 XX PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
 XX PI Rothenberg ME, Zimmerman N;  
 XX DR WPI; 2002-657524/70.  
 XX PT New CC chemokine receptor 3 (CCR3) regulatory site in an untranslated  
 exon 1, exon 2, exon 3 or promoter of a human CCR3 gene or mRNA capable  
 of binding to regulatory elements, useful for preventing e.g. allergic  
 inflammatory reactions.  
 XX PS Disclosure; Fig 4; 56pp; English.

The present sequence represents the promoter of the human CC chemokine  
 receptor 3 (CCR3) gene. CCR3 is expressed on cells involved in allergic  
 and/or inflammatory disorders. The gene comprises 4 exons, with the  
 coding region present on exon 4. The specification describes methods of  
 regulating the expression of CCR3. The regulatory site is derived from an  
 untranslated exon 1, exon 2, exon 3 or promoter of a human CCR3 gene.  
 Regulating the expression of the chemokine receptor CCR3 is useful for  
 preventing or treating disorders involving eosinophils, such as allergic  
 inflammatory and hypersensitivity reactions, certain types of leukemia,  
 and certain infectious disorders involving CCR3, e.g. HIV or respiratory  
 syncytial virus infection. Expression and modulation of CCR3 is a useful  
 tool in assessing eosinophil targeting and in regulating eosinophil-  
 mediated reactions and diseases

Sequence 2895 BP; 829 A; 590 C; 556 G; 920 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 6; Length 2895;  
 Best Local Similarity 100.0%; Pred. No. 0.0015;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGTGCTTATCCGGCAAGAA 22  
 DB 1576 CTTGTGCTTATCCGGCAAGAA 1597

RESULT 6  
 AAT31335  
 ID AAT31335 standard; cDNA; 1193 BP.  
 XX

```

AC AAT31335;
XX
XX
XX 15-NOV-1996 (first entry)
XX
XX CC-chemokine receptor 3 cDNA clone.
XX
XX CC-chemokine receptor 3; CKR-3; Eos-L2; inhibitor; antisense;
XX antiinflammatory; eosinophil; ss.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX CDS 92..1159
XX variation 918..919
XX /*tag= a
XX /*tag= b
XX /note= "CKR-3 cDNA clone has GC at positions 918-919,
XX coding for serine (AGC) at position 276; a genomic clone
XX has GC at these positions, coding for threonine (AGC)"
XX
XX WO9622371-A2.
XX
XX 25-JUL-1996.
XX
XX 19-JAN-1996; 96WO-US000608.
XX
XX 19-JAN-1995; 95US-00375199.
XX
XX (LEUK-) LEUKOSITE INC.
XX (BGHM) BRIGHAM & WOMENS HOSPITAL.
XX (CHIL-) CHILDRENS MEDICAL CENT.
XX
XX Gerard CU, Gerard NP, Mackay CR, Ponath PD, Post TW, Qin S;
XX
XX WPI; 1996-354528/35.
XX P-PSDB; AAW03377.
XX
XX Mammalian chemokine receptor-3 and related nucleic acids - useful to
XX identify receptor inhibitors to treat inflammatory disease, e.g.
XX autoimmune disorders, certain cancers, etc.
XX
XX Claim 1; Page 111-113; 153pp; English.
XX
XX A genomic DNA clone (AAT31335) codes for a novel receptor (AAW03377),
XX designated Eos L2 or C-C chemokine receptor 3 (CKR-3), involved in
XX leukocyte migration associated with inflammation. It was isolated from a
XX human library constructed from eosinophils obtd. from a patient with
XX hyper-eosinophilic syndrome using a probe (p4 cDNA) encoding the MIP-
XX 1alpha/RANTES receptor. A CKR-3 genomic clone (AAT31334) was also
XX isolated, and a consensus sequence is given in AAT31336. The cDNA and
XX genomic clones can be used for the prodn. of recombinant CKR-3 in host
XX cells, or to design antisense sequences useful for treating inflammatory
XX disease
XX
XX Sequence 1193 BP; 274 A; 310 C; 275 G; 334 T; 0 U; 0 Other;
XX
XX Query Match 95.5%; Score 21; DB 2; Length 1193;
XX Best Local Similarity 100.0%; Fred. NO. 0.006;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 TTGTGCTTATCCGGGCAAGAA 22
XX |||||
XX Db 1 TTGTGCTTATCCGGGCAAGAA 21
XX
XX
XX RESULT 7
XX AAV07403
XX ID AAV07403 standard; cDNA; 1193 BP.
XX
XX AC AAV07403;
XX
XX 28-SEP-1998 (first entry)
XX
XX

```

```

DE Human C-C chemokine receptor 3 cDNA.
XX
XX C-C chemokine receptor 3; CKR-3; CCR3; Eos L2; human;
XX G protein-coupled receptor; leukocyte; antibody; antagonist;
XX inflammation; allergy; asthma; graft rejection; infection;
XX autoimmune disease; drug screening; therapy; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 92..1159
XX /*tag= a
XX
XX WO9814480-A1.
XX
XX 09-APR-1998.
XX
XX 24-SEP-1997; 97WO-US017103.
XX
XX 30-SEP-1996; 96US-00720565.
XX
XX (LEUK-) LEUKOSITE INC.
XX
XX Mackay CR, Ponath PD;
XX
XX WPI; 1998-286418/25.
XX P-PSDB; AAW51745.
XX
XX Antibodies to chemokine receptor-3 protein - useful for diagnosis and
XX treatment of inflammatory conditions, e.g. allergy, asthma, autoimmune
XX disease, graft rejection or cancer.
XX
XX Example 8; Page 134-136; 185pp; English.
XX
XX This cDNA codes for novel human C-C chemokine receptor 3 (see AAW51745);
XX also designated CKR-3, CCR3 or Eos L2, that binds and mediates chemotaxis
XX in response to chemokines such as eotaxin, RANTES and MCP-3. The cDNA was
XX isolated from a human eosinophil cDNA library constructed from
XX eosinophils obtained from a patient with hyper-eosinophilic syndrome, and
XX using CKR-1 cDNA as probe. A genomic DNA sequence (see AAV07402) is also
XX provided as well as a consensus sequence (see AAV07404) for CKR-3. The
XX invention relates to isolated and/or recombinant nucleic acids encoding
XX CKR-3, isolated or recombinant CKR-3 polypeptides, recombinant nucleic
XX acid constructs, host cells useful for production of recombinant CKR-3
XX proteins, to antibodies reactive with the receptors, and to methods of
XX using these products to identify ligands, antagonists and agonists of
XX receptor function. Inhibitors of CKR-3 can be used to treat: inflammatory
XX or allergic diseases and conditions, including respiratory allergic
XX diseases such as asthma, allergic rhinitis, hypersensitivity lung
XX disease, hypersensitivity pneumonitis, eosinophilic pneumonia (e.g.
XX Loeffler's syndrome, chronic eosinophilic pneumonia, interstitial lung
XX disease (ILD) e.g. idiopathic pulmonary fibrosis or ILD associated with
XX rheumatoid arthritis, systemic lupus erythematosus, ankylosing
XX spondylitis, systemic sclerosis, Sjogren's syndrome, polymyositis or
XX dermatomyositis), systemic anaphylaxis or hypersensitivity responses,
XX drug allergy, insect sting allergy, inflammatory bowel disease, such as
XX Crohn's disease and ulcerative colitis, spondyloarthritis, scleroderma,
XX psoriasis, inflammatory dermatosis such as dermatitis, eczema, atopic
XX dermatitis, allergic contact dermatitis, urticaria, vasculitis (e.g.
XX necrotizing, cutaneous and hypersensitivity vasculitis); eosinophilic
XX myositis and eosinophilic fasciitis; autoimmune diseases such as
XX rheumatoid arthritis, psoriatic arthritis, multiple sclerosis, systemic
XX lupus erythematosus, myasthenia gravis, juvenile onset diabetes, graft
XX glomerulonephritis, autoimmune thyroiditis and Behcet's disease; graft
XX rejection, including allograft rejection or graft-versus-host disease;
XX cancers with leukocyte infiltration of the skin or organs; and also
XX reperfusion injury, atherosclerosis, certain haematologic malignancies,
XX septic shock and endotoxin shock. Promoters of CKR-3 function can be used
XX for treating immunosuppression e.g. in AIDS patients or individuals
XX undergoing radiation therapy, chemotherapy, therapy for autoimmune
XX disease or other drug therapy, and immunosuppression due congenital
XX deficiency in receptor function or other causes; and infectious diseases
XX such as parasitic diseases, including helminth infections, such as

```

CC nematodes (round worms). The agents can also be used for detection and  
CC diagnosis  
CC  
SQ Sequence 1193 BP; 274 A; 310 C; 275 G; 334 T; 0 U; 0 Other;  
Query Match 95.5%; Score 21; DB 2; Length 1193;  
Best Local Similarity 100.0%; Pred. No. 0.006;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 TTGTGCTTATCGGGCAAGAA 22  
DB 1 TTGTGCTTATCGGGCAAGAA 21  
RESULT 8  
ID ABX50975/c  
XX ABX50975 standard; cDNA; 265 BP.  
AC ABX50975;  
XX  
DT 25-FEB-2003 (first entry)  
DE Bovine EST associated with lactation/muscle/fat deposition #904.  
XX  
XX Bovine; ss; EST; expressed sequence tag; lactation; LMFD;  
KW muscle deposition; fat deposition; genome mapping; gene identification;  
KW gene analysis; cattle breeding.  
XX  
OS Bos Taurus.  
XX  
PN US2002137160-A1.  
XX  
PD 26-SEP-2002.  
XX  
PF 26-OCT-2001; 2001US-00983965.  
XX  
PR 17-DEC-1998; 98US-0113678P.  
PR 15-DEC-1999; 99US-00465231.  
XX  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
XX  
PI Byatt JC, Mathialagan N, Tao N, Warren WC;  
XX WPI; 2003-102386/09.  
XX  
PT Purified nucleic acid molecules, useful for genome mapping, gene  
PT identification and analysis, cattle breeding or preparation of constructs  
PT for cattle gene expression and genetically improved cattle.  
XX  
PS Claim 2; SEQ ID NO 904; 38pp; English.  
XX  
CC The invention relates to a purified nucleic acid molecule associated with  
CC lactation or muscle and fat deposition (designated LMFD), derived from  
CC cattle, and the LMFD nucleic acid can specifically hybridise to a second  
CC nucleic acid molecule comprising any of 5912 nucleotide sequences,  
CC appearing as ABX50072-ABX55983, or complements of them. Also included are  
CC (1) a transformed cell having a nucleic acid comprising an LMFD nucleic  
CC acid linked to a promoter and a 3' non-translated sequence that  
CC functions in the cell to cause termination of transcription and addition  
CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and  
CC (2) determining a level or pattern of a molecule in a bovine cell or  
CC tissue comprising: (a) incubating a marker nucleic acid (comprising any  
CC of the 5912 nucleic acid sequences or its complement or fragment) with a  
CC complementary nucleic acid molecule obtained from the bovine cell or  
CC tissue, where hybridisation between the marker nucleic acid and the  
CC complementary nucleic acid permits the detection of the molecule; and (b)  
CC detecting the level or pattern of the complementary nucleic acid, where  
CC the detection of the complementary nucleic acid is predictive of the  
CC level or pattern of the molecule. The LMFD nucleic acid is used for  
CC determining a level or pattern of a molecule in a bovine cell or tissue.

CC It is useful for genome mapping, gene identification and analysis, cattle  
CC breeding, preparation of constructs for use in cattle gene expression, or  
CC for genetically improving cattle. The present sequence is one of the 5912  
CC bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The present  
CC sequence was not shown in the specification but was obtained in  
CC electronic format from the USPTO web site:  
CC seqdata.uspto.gov/sequence.html?DocID=20020137160  
XX  
SQ Sequence 265 BP; 67 A; 72 C; 67 G; 59 T; 0 U; 0 Other;  
Query Match 72.7%; Score 16; DB 7; Length 265;  
Best Local Similarity 100.0%; Pred. No. 6;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTTGTGCTTATCGGG 16  
DB 217 CTTGTGCTTATCGGG 202  
RESULT 9  
ID ABL17664/c  
XX ABL17664 standard; DNA; 23654 BP.  
AC ABL17664;  
XX  
DT 26-MAR-2002 (first entry)  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 4465.  
XX  
XX Drosophila; developmental biology; cell signalling; insecticide;  
KW pharmaceutical; gene; ds.  
XX  
OS Drosophila melanogaster.  
XX  
PN WO200171042-A2.  
XX  
PD 27-SEP-2001.  
XX  
PF 23-MAR-2001; 2001WO-US009231.  
XX  
PR 23-MAR-2000; 2000US-0191637P.  
PR 11-JUL-2000; 2000US-00614150.  
XX  
PA (PEKE) PE CORP NY.  
XX  
PI Venter JC, Adams M, Li PWD, Myers EW;  
XX WPI; 2001-656860/75.  
XX  
PS New isolated nucleic acid detection reagent for detecting 1000 or more  
PS genes from Drosophila and for elucidating cell signalling and cell-cell  
PS interactions.  
XX  
PS Claim 1; SEQ ID NO 4465; 21pp + Sequence Listing; English.  
XX  
CC The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from Drosophila. The invention is  
CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABBS57737-  
CC ABBS72072). The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 23654 BP; 6479 A; 5244 C; 5233 G; 6698 T; 0 U; 0 Other;  
Query Match 68.2%; Score 15; DB 4; Length 23654;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 8 TTATCCGGCAAGAA 22

Db 20478 TTATCCGGGCAAGNA 20464

|||||

RESULT 10  
ADB12176/c  
ID ADB12176 standard; DNA; 438 BP.

XX AC ADB12176;

XX DT 20-NOV-2003 (first entry)

XX DE Alloicoccus otitis antigenic protein encoding DNA SEQ ID NO:6539.

XX KW Alloicoccus otitidis; antigenic protein; immunogenic; immunisation;  
XX gene therapy; Gram-positive bacterium; infection; gene; ds.

XX OS Alloicoccus otitis.

XX PN WO2003048304-A2.

XX PD 12-JUN-2003.

XX PF 25-NOV-2002; 2002WO-US036123.

XX PR 29-NOV-2001; 2001US-0333777P.

XX PR 18-NOV-2002; 2002US-0426742P.

XX PA (AMHP) WYETH HOLDINGS CORP.

XX PI Fletcher LD, McMichael JC, Russell DP, Zagursky RJ;

XX WPI; 2003-505284/47.

XX P-PSDB; ADB12173.

XX PT New alloicoccus otitidis polynucleotides and polypeptides, useful for  
PT treating and diagnosing diseases, drug screening assays and monitoring of  
PT effects during drug clinical trials.

XX PS Claim 7; SEQ ID NO 6539; 1019pp; English.

XX The present invention describes an isolated polynucleotide (I) of  
CC Alloicoccus otitidis genomic DNA, which encodes an antigenic protein.  
CC Alloicoccus otitidis is a gram-positive bacterium. Also described: (1)  
CC an isolated polypeptide that is encoded by the polynucleotide (I); (2) an  
CC expression vector comprising the novel isolated polynucleotide (I), its  
CC complement, degenerate variant or fragment; (3) a genetically engineered  
CC host cell, transfected, transformed or infected with the vector of (2);  
CC (4) an antibody specific for the polypeptide of (1); (5) an immunogenic  
CC composition comprising the polypeptide, its complement, biological  
CC equivalent or fragment, or the polynucleotide that is comprised in the  
CC expression vector; (6) a pharmaceutical composition comprising the  
CC polypeptide of (1) and a carrier; (7) a protein chip comprising an array  
CC of the polypeptides of (1), their biological equivalent or fragment; (8)  
CC immunising against Alloicoccus otitidis by administering to a host the  
CC immunogenic composition; (9) detecting and/or identifying Alloicoccus  
CC otitidis in the biological sample; (10) a kit comprising a container  
CC containing the novel polynucleotide, its degenerate variant or fragment,  
CC or the antibody of (4); and (11) producing a polypeptide by culturing the  
CC genetically engineered host cell under conditions suitable to produce the  
CC polypeptide from the culture. (I) can be used in gene therapy. The  
CC polynucleotides, polypeptides, antibodies and compositions of the present  
CC invention can be used for treating and diagnosing diseases, drug  
CC screening assays and monitoring of effects during drug clinical trials.  
CC The polynucleotides are useful for expressing and detecting Alloicoccus  
CC otitidis. The present sequence encodes an Alloicoccus otitidis antigen  
CC protein from the present invention.

XX SQ Sequence 438 BP; 119 A; 106 C; 108 G; 105 T; 0 U; 0 Other;

Query Match

63.6%; Score 14; DB 8; Length 438;

Best Local Similarity 100.0%; Pred. No. 93;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTGTGCTTATCCGG 15  
| | | | | | | | | |  
Db 232 TTGTGCTTATCCGG 219

RESULT 11

ABK75795

ID ABK75795 standard; DNA; 717 BP.

XX AC

XX AC ABK75795;

XX DT 13-AUG-2002 (first entry)

XX DE Bacillus licheniformis genomic sequence tag (GST) #3086.

XX KW Differential gene expression; genomic sequenced tag; GST;  
KW altered culture condition; environmental stress;  
KW physiological provocation; ds.

XX OS Bacillus licheniformis.

XX PN WO200229113-A2.

XX PD 11-APR-2002.

XX PF 05-OCT-2001; 2001WO-US031437.

XX PR 06-OCT-2000; 2000US-00680598.

XX PR 27-MAR-2001; 2001US-0279526P.

XX PA (NOVO) NOVOZYMES BIOTECH INC.

XX PA (NOVO) NOVOZYMES AS.

XX PI Berka R, Clausen IG;

XX WPI; 2002-416684/44.

XX Monitoring differential expression of several genes in first Bacillus  
PT cell relative to expression of same genes in one or more second Bacillus  
PT cells, by using substrate containing Bacillus genomic sequenced tag  
PT array.

XX Claim 4; SEQ ID NO 3086; 200pp; English.

XX The invention describes a method of monitoring differential expression of  
CC genes in a first Bacillus cell relative to expression of the genes in  
CC other Bacillus cells, comprising hybridising labelled nucleic acid probes  
CC isolated from Bacillus cells to a substrate containing array of Bacillus  
CC genomic sequenced tags (GST), examining the array, and determining  
CC relative gene expression by an observed hybridisation reporter signal of  
CC a spot in the array. The method is useful for measuring the expression of  
CC genes in a first Bacillus cell relative to expression of the same genes  
CC in one or more second Bacillus cells. The method is useful for monitoring  
CC global expression of several genes from a Bacillus cell, discovering new  
CC genes, identifying possible functions of unknown open reading frames and  
CC monitoring gene copy number, variation and stability. Monitoring changes  
CC in expression of genes may be used to provide a representation of the way  
CC in which Bacillus cells adapt to changes in culture conditions,  
CC environmental stress or other physiological provocation. Extensive follow  
CC up characterisation is unnecessary, when one spot on an array equals one  
CC gene or one open reading frame, since sequence information is available.  
CC This sequence represents a genomic sequence tag (GST) used in the method  
CC of the invention. Note: The sequence data for this patent did not form  
CC part of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 717 BP; 189 A; 165 C; 175 G; 188 T; 0 U; 0 Other;

Query Match

63.6%; Score 14; DB 6; Length 717;

Best Local Similarity 100.0%; Pred. No. 92;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 5 TGCTTATCCGGCA 18  
Db 373 TGCTTATCCGGCA 386

RESULT 12

AA91767  
ID AAX91767 standard; DNA; 945 BP.

XX AC AAX91767;  
XX DT 27-AUG-2003 (revised)  
XX DT 20-MAR-2003 (revised)  
XX DT 25-AUG-1999 (first entry)  
XX DE Porphyromonas gingivalis protein PG78 encoding DNA.  
XX DE Porphyromonas gingivalis; PG; periodontal disease; gingivitis; vaccine;  
XX KW antigenic; ds.  
XX OS Porphyromonas gingivalis.  
XX PN WO9929870-A1.  
XX PD 17-JUN-1999.  
XX PF 10-DEC-1998; 98WO-AU001023.  
XX PR 10-DEC-1997; 97AU-00000839.  
XX PR 31-DEC-1997; 97AU-00001182.  
XX PR 30-JAN-1998; 98AU-00001546.  
XX PR 10-MAR-1998; 98AU-00002264.  
XX PR 09-APR-1998; 98AU-00002911.  
XX PR 23-APR-1998; 98AU-00003128.  
XX PR 05-MAY-1998; 98AU-00003338.  
XX PR 22-JUL-1998; 98AU-00004917.  
XX PR 04-AUG-1998; 98AU-00005028.  
XX PA (CSLC-) CSL LTD.  
XX PI Ross BC, Barr IG, Patterson MA, Agius CT, Rothel LJ, Margetts MB;  
XX PI Hocking DM, Webb EA;  
XX WPI; 1999-385613/32.  
XX DR P-PSDB; AAX34549.  
XX PT Antigenic Porphyromonas gingivalis peptides for preventing gingivitis.  
XX PS Claim 12; Page 253-254; 588pp; English.

XX CC AAX91536 to AAX91801 encode two hundred and sixty six antigenic  
XX CC Porphyromonas gingivalis (PG) polypeptide sequences given in AAX34318 to  
XX CC AAX34583. AAX91802 to AAX91989 represent PCR primers used in the  
XX CC isolation of the PG polypeptides. The PG polypeptides have antibacterial  
XX CC activity with a vaccine mechanism of action. The PG polypeptides can be  
XX CC used as vaccines especially against Porphyromonas gingivalis. Probes can  
XX CC be used to detect Porphyromonas gingivalis in standard hybridisation  
XX CC assays. Porphyromonas gingivalis is involved in periodontal disease  
XX CC especially gingivitis. (Updated on 20-MAR-2003 to correct PR field.)  
XX SQ Sequence 945 BP; 207 A; 245 C; 226 G; 267 T; 0 U; 0 Other;  
Query Match 63.6%; Score 14; DB 2; Length 945;  
Best Local Similarity 100.0%; Pred. No. 92;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CTTATCCGGCAAG 20  
Db 710 CTTATCCGGCAAG 723

RESULT 13

AA91633  
ID AAX91633 standard; DNA; 987 BP.

XX AC AAX91633;  
XX DT 27-AUG-2003 (revised)  
XX DT 20-MAR-2003 (revised)  
XX DT 25-AUG-1999 (first entry)  
XX DE Porphyromonas gingivalis protein PG78 ORF encoding DNA.  
XX DE Porphyromonas gingivalis; PG; periodontal disease; gingivitis; vaccine;  
XX KW antigenic; ds.  
XX OS Porphyromonas gingivalis.  
XX PN WO9929870-A1.  
XX PD 17-JUN-1999.  
XX PF 10-DEC-1998; 98WO-AU001023.  
XX PR 10-DEC-1997; 97AU-00000839.  
XX PR 31-DEC-1997; 97AU-00001182.  
XX PR 30-JAN-1998; 98AU-00001546.  
XX PR 10-MAR-1998; 98AU-00002264.  
XX PR 09-APR-1998; 98AU-00002911.  
XX PR 23-APR-1998; 98AU-00003128.  
XX PR 05-MAY-1998; 98AU-00003338.  
XX PR 22-JUL-1998; 98AU-00004917.  
XX PR 04-AUG-1998; 98AU-00005028.  
XX PA (CSLC-) CSL LTD.  
XX PI Ross BC, Barr IG, Patterson MA, Agius CT, Rothel LJ, Margetts MB;  
XX PI Hocking DM, Webb EA;  
XX WPI; 1999-385613/32.  
XX DR P-PSDB; AAX34415.  
XX PT Antigenic Porphyromonas gingivalis peptides for preventing gingivitis.  
XX PS Claim 12; Page 162; 588pp; English.

XX CC AAX91536 to AAX91801 encode two hundred and sixty six antigenic  
XX CC Porphyromonas gingivalis (PG) polypeptide sequences given in AAX34318 to  
XX CC AAX34583. AAX91802 to AAX91989 represent PCR primers used in the  
XX CC isolation of the PG polypeptides. The PG polypeptides have antibacterial  
XX CC activity with a vaccine mechanism of action. The PG polypeptides can be  
XX CC used as vaccines especially against Porphyromonas gingivalis. Probes can  
XX CC be used to detect Porphyromonas gingivalis in standard hybridisation  
XX CC assays. Porphyromonas gingivalis is involved in periodontal disease  
XX CC especially gingivitis. (Updated on 20-MAR-2003 to correct PR field.)  
XX SQ Sequence 987 BP; 215 A; 258 C; 239 G; 275 T; 0 U; 0 Other;

Query Match 63.6%; Score 14; DB 2; Length 987;  
Best Local Similarity 100.0%; Pred. No. 92;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 CTTATCCGGCAAG 20  
Db 752 CTTATCCGGCAAG 765

RESULT 14

AA90227/c  
ID AAV80227 standard; DNA; 1262 BP.

```

XX AC AAV80227;
XX DT 02-MAR-1999 (first entry)
XX DE Maize globulin promoter sequence.
XX KW Maize; acyl-ACP thioesterase; enzyme; oleoyl-ACP thioesterase; OTE; PTE;
XX KW palmitoyl-ACP thioesterase; transgenic plant; oil; fatty acid; promoter;
XX KW regulatory element; transcriptional terminator; globulin; ss.
XX OS Zea mays.
XX PN W09850569-A2.
XX PD 12-NOV-1998.
XX XX
XX PF 22-APR-1998; 98WO-US008097.
XX PR 05-MAY-1997; 97US-0045827P.
XX PA (DOWC ) DOW AGROSCIENCES LLC.
XX PI Rubin-Wilson B, Guo L, Skokut T, Young S, Folkerts O;
XX PI Armstrong K, Cowen NM;
XX DR WPI; 1999-034732/03.
XX XX
XX PT Composition comprising a promoter regulatory element, acyl-ACP
XX PT thioesterase coding sequence, and a terminator - useful for, e.g.
XX PT production of plant oil with an altered fatty acid content.
XX PS Claim 2; Page 142-144; 179pp; English.
XX CC The invention relates to genes encoding maize acyl-ACP thioesterase
XX CC enzymes. The enzymes especially, oleoyl-ACP thioesterase (OTE) and
XX CC palmitoyl-ACP thioesterase (PTE) can be used to create transgenic plants
XX CC having altered oil profiles. The invention provides a composition
XX CC comprising in a 5' to 3' direction: (i) a promoter regulatory element;
XX CC (ii) an acyl-ACP thioesterase encoding nucleic acid isolated from maize;
XX CC and (iii) a transcriptional terminator. The compositions and plant cell
XX CC of comprising the compositions can be used to produce plant oil having
XX CC altered levels of fatty acids. The present sequence represents the maize
XX CC globulin promoter sequence
XX SQ Sequence 1262 BP; 380 A; 288 C; 248 G; 346 T; 0 U; 0 Other;

Query Match 63.6%; Score 14; DB 2; Length 1262;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTGCTTATCGGGC 17
DB 1069 GTGCTTATCGGGC 1056

RESULT 15
ABA94959/c
ID ABA94959 standard; DNA; 1262 BP.
XX AC ABA94959;
XX DT 08-MAY-2002 (first entry)
XX DE Globulin seed specific promoter fragment.
XX KW Beta-ketoacyl-acyl carrier protein synthase II; KAS II; maize; soybean;
XX KW oil; fatty acid; transgenic; plant; globulin; promoter; ds.
XX OS Synthetic.
XX PN US6323395-B1.

```

```

PD 27-NOV-2001.
XX XX
XX PF 16-DEC-1998; 98US-00212609.
XX PR 24-DEC-1997; 97US-0068784P.
XX PA (DOWC ) DOW AGROSCIENCES LLC.
XX PI Rubin-Wilson BC, Young SA, Folkerts O;
XX DR WPI; 2002-178575/23.
XX XX
XX PT New DNA construct useful as vector to transform plants, particularly
XX PT corn, with modified saturated fat content contains nucleic acid encoding
XX PT beta-ketoacyl-acyl carrier protein synthase II isolated from maize or
XX PT soybean.
XX PS Example 7; Col 83-84; 44pp; English.
XX CC The invention relates to genes encoding beta-ketoacyl-acyl carrier
XX CC protein synthase II (KAS II) isolated from maize or soybean tissues. The
XX CC saturate levels of oils found in plant cells can be altered by modifying
XX CC the expression and activity levels of KAS II within the cell. A DNA
XX CC construct comprising in the 5' to 3' direction, a promoter regulatory
XX CC element, a nucleic acid fragment encoding KAS II and a transcriptional
XX CC terminator can be used to modify the saturated fat content of transgenic
XX CC plants, particularly corn. The present sequence represents a globulin
XX CC seed specific promoter fragment used in the construction of
XX CC transformation vectors
XX SQ Sequence 1262 BP; 380 A; 288 C; 248 G; 346 T; 0 U; 0 Other;

Query Match 63.6%; Score 14; DB 6; Length 1262;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTGCTTATCGGGC 17
DB 1069 GTGCTTATCGGGC 1056

Search completed: August 2, 2004, 18:24:27
Job time : 109.207 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 2, 2004, 17:27:15 ; Search time 492.914 seconds  
(without alignments)  
1934.510 Million cell updates/sec

Title: US-10-068-067-18  
Perfect score: 22  
Sequence: 1 cttgtgttatccgggcaaga 22

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb.ba.\*
- 2: gb.htg.\*
- 3: gb.in.\*
- 4: gb.om.\*
- 5: gb.ov.\*
- 6: gb.pat.\*
- 7: gb.ph.\*
- 8: gb.pl.\*
- 9: gb.pr.\*
- 10: gb.ro.\*
- 11: gb.sts.\*
- 12: gb.sy.\*
- 13: gb.un.\*
- 14: gb.vi.\*
- 15: em.ba.\*
- 16: em.fun.\*
- 17: em.hum.\*
- 18: em.in.\*
- 19: em.mu.\*
- 20: em.om.\*
- 21: em.or.\*
- 22: em.ov.\*
- 23: em.pat.\*
- 24: em.ph.\*
- 25: em.pl.\*
- 26: em.ro.\*
- 27: em.sts.\*
- 28: em.un.\*
- 29: em.vi.\*
- 30: em.htg.hum.\*
- 31: em.htg.inv.\*
- 32: em.htg.other.\*
- 33: em.htg.mus.\*
- 34: em.htg.pln.\*
- 35: em.htg.rod.\*
- 36: em.htg.mam.\*
- 37: em.htg.vrt.\*
- 38: em.py.\*
- 39: em.htgo.hum.\*
- 40: em.htgo.mus.\*
- 41: em.htgo.other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	22	100.0	22	6	AX513219	AX513219 Sequence
2	22	100.0	22	6	AX513224	AX513224 Sequence
3	22	100.0	51	6	AX513217	AX513217 Sequence
4	22	100.0	51	6	AX513222	AX513222 Sequence
5	22	100.0	212	9	AF262303	AF262303 Homo sapi
6	22	100.0	260	9	AF224495	AF224495 Homo sapi
7	22	100.0	348	9	AF262299	AF262299 Homo sapi
8	22	100.0	406	9	AF262301	AF262301 Homo sapi
9	22	100.0	410	9	AF262302	AF262302 Homo sapi
10	22	100.0	436	9	AF262304	AF262304 Homo sapi
11	22	100.0	957	9	AF224496S1	AF224496 Homo sapi
12	22	100.0	1453	9	AF247360	AF247360 Homo sapi
13	22	100.0	2895	6	AX513212	AX513212 Sequence
14	22	100.0	2895	9	AF237380S1	AF237380 Homo sapi
15	22	100.0	177334	9	AC138069	AC138069 Homo sapi
16	22	100.0	197279	9	AC104439	AC104439 Homo sapi
17	22	100.0	220965	2	HSA312688	AJ312688 Homo sapi
18	21	95.5	1193	6	AR300122	AB300122 Sequence
19	21	95.5	1193	6	BD882061	BD882061 G-protein
20	18	81.8	31654	3	CEC32H11	282260 Caenorhabdi
21	17	77.3	1454	9	AF247359	AF247359 Homo sapi
22	16	72.7	45336	10	AL935309	AL935309 Mouse DNA
23	16	72.7	165837	2	AC101908	AC101908 Mus muscu
24	16	72.7	218358	2	AC145931	AC145931 Gallus ga
25	16	72.7	235349	2	AC109855	AC109855 Rattus no
26	15	68.2	4161	1	BSF133614	AJ133614 Bacillus
27	15	68.2	61421	2	AC103765	AC103765 Homo sapi
28	15	68.2	76854	3	AC003052	AC003052 Drosophil
29	15	68.2	83991	8	AP004965	AP004965 Lotus cor
30	15	68.2	86398	2	AC017785	AC017785 Drosophil
31	15	68.2	133974	2	AC108894	AC108894 Bos tauru
32	15	68.2	157533	2	AC133903	AC133903 Mus muscu
33	15	68.2	158113	4	AC136966	AC136966 Bos tauru
34	15	68.2	166537	2	AC131916	AC131916 Mus muscu
35	15	68.2	167201	3	AC092397	AC092397 Drosophil
36	15	68.2	176486	8	AP003768	AP003768 Oryza sat
37	15	68.2	188654	2	AC136320	AC136320 Mus muscu
38	15	68.2	197461	2	AC134814	AC134814 Rattus no
39	15	68.2	221649	2	AC147442	AC147442 Gallus ga
40	15	68.2	232049	2	AC127108	AC127108 Rattus no
41	15	68.2	235572	2	AC134470	AC134470 Mus muscu
42	15	68.2	246237	3	CEY39B6A	AL132948 Caenorhab
43	15	68.2	260139	3	AE003614	AE003614 Drosophil
44	15	68.2	305961	1	AE016937	AE016937 Bacteroid
45	15	68.2	339977	2	AC109846	AC109846 Rattus no

ALIGNMENTS

RESULT 1  
AX513219  
LOCUS AX513219 22 bp DNA linear PAT 03-OCT-2002  
DEFINITION Sequence 18 from Patent WO02062848.  
ACCESSION AX513219  
VERSION AX513219.1 GI:23504282  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Rothenberg, M.E. and Zimmerman, N.  
TITLE Regulation of cc chemokine receptor 3 (ccr3) expression  
JOURNAL Patent: WO 02062848-A 18 15-AUG-2002;

## CHILDREN'S HOSPITAL MEDICAL CENTER (US)

FEATURES  
source

Location/Qualifiers  
1. .22  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

## ORIGIN

Query Match 100.0%; Score 22; DB 6; Length 22;

Best Local Similarity 100.0%; Pred. No. 0.048; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGTGCTTATCCGGCAAGAA 22

Db 1 CTTGTGCTTATCCGGCAAGAA 22

## RESULT 2

AX513224 LOCUS AX513224 22 bp RNA linear PAT 03-OCT-2002

DEFINITION Sequence 23 from Patent WO02062848.

ACCESSION AX513224

VERSION AX513224.1 GI:23504287

KEYWORDS

SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 Rothenberg,M.E. and Zimmerman,N.

TITLE Regulation-of-cc-chemokine receptor 3 (ccr3) expression

JOURNAL Patent: WO 02062848-A 23 15-AUG-2002;

CHILDREN'S HOSPITAL MEDICAL CENTER (US)

## FEATURES

Location/Qualifiers  
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/mol\_type="unassigned RNA"  
/db\_xref="taxon:9606"

## ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.048; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGTGCTTATCCGGCAAGAA 22

Db 1 CTTGTGCTTATCCGGCAAGAA 22

## RESULT 3

AX513217 LOCUS AX513217 51 bp DNA linear PAT 03-OCT-2002

DEFINITION Sequence 16 from Patent WO02062848.

ACCESSION AX513217

VERSION AX513217.1 GI:23504280

KEYWORDS

SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 Rothenberg,M.E. and Zimmerman,N.

TITLE Regulation of cc chemokine receptor 3 (ccr3) expression

JOURNAL Patent: WO 02062848-A 16 15-AUG-2002;

CHILDREN'S HOSPITAL MEDICAL CENTER (US)

## FEATURES

Location/Qualifiers  
1. .51  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

## ORIGIN

Query Match 100.0%; Score 22; DB 6; Length 51;

Best Local Similarity 100.0%; Pred. No. 0.043;

Mismatches 22; Conservative 0; Indels 0; Gaps 0;

QY 1 CTTGTGCTTATCCGGCAAGAA 22

Db 1 CTTGTGCTTATCCGGCAAGAA 37

## RESULT 4

AX513222 LOCUS AX513222 51 bp RNA linear PAT 03-OCT-2002

DEFINITION Sequence 21 from Patent WO02062848.

ACCESSION AX513222

VERSION AX513222.1 GI:23504285

KEYWORDS

SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 Rothenberg,M.E. and Zimmerman,N.

TITLE Regulation of cc chemokine receptor 3 (ccr3) expression

JOURNAL Patent: WO 02062848-A 21 15-AUG-2002;

CHILDREN'S HOSPITAL MEDICAL CENTER (US)

## FEATURES

Location/Qualifiers  
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/mol\_type="unassigned RNA"  
/db\_xref="taxon:9606"

## ORIGIN

Query Match 100.0%; Score 22; DB 6; Length 51;

Best Local Similarity 100.0%; Pred. No. 0.043;

Mismatches 22; Conservative 0; Indels 0; Gaps 0;

QY 1 CTTGTGCTTATCCGGCAAGAA 22

Db 1 CTTGTGCTTATCCGGCAAGAA 37

## RESULT 5

AF262303 LOCUS AF262303 212 bp mRNA linear PRI 26-JUN-2002

DEFINITION Homo sapiens clone 6 CC chemokine receptor 3 (CCR3) mRNA, partial

CDS.

ACCESSION AF262303

VERSION AF262303.1 GI:19171648

KEYWORDS

SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 212)

Vijh,S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and

Michael,N.L.

TITLE Transcription Regulation of Human Chemokine Receptor CCR3: Evidence

for a Rare TATA-less Promoter Structure Conserved between

Drosophila and Humans

JOURNAL Genomics 80 (1), 86-95 (2002)

MEDLINE 22074933

PUBMED 12079287

REFERENCE 2 (bases 1 to 212)

Vijh,S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.

TITLE Direct Submission

JOURNAL Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis,

Walter Reed Army Institute of Research, 1600 E. Gude Drive,

Rockville, MD 20850, USA

FEATURES

Location/Qualifiers  
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/db\_xref="taxon:9606"  
/chromosome="3"

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/clone="6"
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150. >212
/gene="CCR3"
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CD8 lymphocytes, microglia, dendritic cells, and
monocytes"
/codon_start=1
/product="CC chemokine receptor 3"
/protein_id="AAL85632.1"
/db_xref="GI:19171649"
/translation="MTISLDIVETFGTTSYDDVG"

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Query Match 100.0%; Score 22; DB 9; Length 212;
Best Local Similarity 100.0%; Pred. No. 0.036;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGTGCTTATCCGGCAAGAA 22
DB 12 CTTGTGCTTATCCGGCAAGAA 33

RESULT 6
LOCUS AF224495 260 bp mRNA linear PRI 02-MAY-2001
DEFINITION Homo sapiens CC chemokine receptor 3 (CCR3) mRNA, partial cds.
ACCESSION AF224495
VERSION AF224495.1 GI:13924481
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 260)
AUTHORS Scotet,E.J.
TITLE CCR3 expression is associated with chromatin remodeling in Th2
cells
JOURNAL Unpublished
2 (bases 1 to 260)
AUTHORS Scotet,E.J.
DIRECT SUBMISSION
TITLE Direct Submission
JOURNAL Submitted (13-JAN-2000) Basel Institute for Immunology, 487
Grenzacherstrasse, Basel CH-4005, Switzerland
FEATURES
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/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_type="T cell"
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/gene="CCR3"
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/codon_start=1
/product="CC chemokine receptor 3"
/protein_id="AAK49027.1"
/db_xref="GI:13924482"
/translation="MTISLDIVETFGTTSYDDVGLLCEKADTRALMAQFVPPLYSLV
FTVGLLGNVVVV"

ORIGIN
Query Match 100.0%; Score 22; DB 9; Length 260;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGTGCTTATCCGGCAAGAA 22
DB 13 CTTGTGCTTATCCGGCAAGAA 34

RESULT 7
LOCUS AF262299 348 bp mRNA linear PRI 26-JUN-2002
DEFINITION Homo sapiens clone 1 CC chemokine receptor 3 (CCR3) mRNA, partial
cds.
ACCESSION AF262299
VERSION AF262299.1 GI:19171640
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 348)
AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Iman,Z., Ehrenberg,P.K. and
Michael,N.L.
TITLE Transcription Regulation of Human Chemokine Receptor CCR3: Evidence
for a Rare TATA-less Promoter Structure Conserved between
Drosophila-and-Humans.
JOURNAL Genomics 80 (1), 86-95 (2002)
MEDLINE 22074933
PUBMED 12079287
2 (bases 1 to 348)
AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.
DIRECT SUBMISSION
TITLE Direct Submission
JOURNAL Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis,
Walter Reed Army Institute of Research, 1600 E. Gude Drive,
Rockville, MD 20850, USA
FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="3"
/map="3p21"
/clone="1"
/cell_type="eosinophil"
1..>348
/gene="CCR3"
120..>348
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/notes="G-protein coupled receptor; principal ectoxin
receptor expressed on eosinophils, CD4 Th2 lymphocytes,
CD8 lymphocytes, microglia, dendritic cells, and
monocytes"
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/product="CC chemokine receptor 3"
/protein_id="AAL85628.1"
/db_xref="GI:19171641"
/translation="MTISLDIVETFGTTSYDDVGLLCEKADTRALMAQFVPPLYSLV
FTVGLLGNVVVVMLIKYRRLIMINILNL"

ORIGIN
Query Match 100.0%; Score 22; DB 9; Length 348;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGTGCTTATCCGGCAAGAA 22
DB 42 CTTGTGCTTATCCGGCAAGAA 63

RESULT 8
LOCUS AF262301 406 bp mRNA linear PRI 26-JUN-2002
DEFINITION Homo sapiens clone 4 CC chemokine receptor 3 (CCR3) mRNA, partial
cds.
ACCESSION AF262301
VERSION AF262301.1 GI:19171644
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 406)  
 Vjrh.S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and  
 Michael,N.L.  
 Transcription Regulation of Human Chemokine Receptor CCR3: Evidence  
 for a Rare TATA-less Promoter Structure Conserved between  
 Drosophila and Humans  
 Genomics 80 (1), 86-95 (2002)  
 22074933  
 MEDLINE  
 12079287  
 PUBLISHED  
 REFERENCE  
 2 (bases 1 to 406)  
 Vjrh.S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.  
 Direct Submission  
 TITLS  
 JOURNAL  
 Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis,  
 Walter Reed Army Institute of Research, 1600 E. Gude Drive,  
 Rockville, MD 20850, USA  
 Location/Qualifiers  
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 /db\_xref="taxon:9606"  
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 CD8 lymphocytes, microglia, dendritic cells, and  
 monocytes"  
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 /product="CC chemokine receptor 3"  
 /protein\_id="AAL85630.1"  
 /db\_xref="GI:19171645"  
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 FTVGLLGNVVVMILIKYRRLRIMTNILNLAISDQG"  
 ORIGIN  
 Query Match 100.0%; Score 22; DB 9; Length 406;  
 Best Local Similarity 100.0%; Pred. No. 0.034;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CTTGTGCTTATCCGGCAAGAA 22  
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 Db 13 CTTGTGCTTATCCGGCAAGAA 34  
 |||||  
 RESULT 9  
 AF262302  
 LOCUS  
 DEFINITION Homo sapiens clone 5 CC chemokine receptor 3 (CCR3) mRNA, partial  
 cds.  
 ACCESSION AF262302  
 VERSION AF262302.1 GI:19171646  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 410)  
 Vjrh.S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and  
 Michael,N.L.  
 Transcription Regulation of Human Chemokine Receptor CCR3: Evidence  
 for a Rare TATA-less Promoter Structure Conserved between  
 Drosophila and Humans  
 Genomics 80 (1), 86-95 (2002)  
 22074933  
 MEDLINE  
 12079287  
 PUBLISHED  
 REFERENCE  
 2 (bases 1 to 410)  
 Vjrh.S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.  
 Direct Submission  
 TITLS  
 JOURNAL  
 Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis,  
 Walter Reed Army Institute of Research, 1600 E. Gude Drive,  
 Rockville, MD 20850, USA  
 Location/Qualifiers  
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 /db\_xref="taxon:9606"  
 /chromosome="3"  
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 /cell\_type="primary eosinophil"  
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 170. .>410  
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 receptor expressed on eosinophils, CD4 Th2 lymphocytes,  
 CD8 lymphocytes, microglia, dendritic cells, and  
 monocytes"  
 /codon\_start=1  
 /product="CC chemokine receptor 3"  
 /protein\_id="AAL85631.1"  
 /db\_xref="GI:19171647"  
 /translation="MTSLDTVETFGTTSYDDVGLLCEKADTRALMAQFVPPYLSLV  
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 ORIGIN  
 Query Match 100.0%; Score 22; DB 9; Length 410;  
 Best Local Similarity 100.0%; Pred. No. 0.033;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CTTGTGCTTATCCGGCAAGAA 22  
 |||||  
 Db 13 CTTGTGCTTATCCGGCAAGAA 34  
 |||||  
 RESULT 10  
 AF262304  
 LOCUS  
 DEFINITION Homo sapiens clone 7 CC chemokine receptor 3-like mRNA, partial  
 sequence, alternatively spliced.  
 ACCESSION AF262304  
 VERSION AF262304.1 GI:19171650  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 436)  
 Vjrh.S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and  
 Michael,N.L.  
 Transcription Regulation of Human Chemokine Receptor CCR3: Evidence  
 for a Rare TATA-less Promoter Structure Conserved between  
 Drosophila and Humans  
 Genomics 80 (1), 86-95 (2002)  
 22074933  
 MEDLINE  
 12079287  
 PUBLISHED  
 REFERENCE  
 2 (bases 1 to 436)  
 Vjrh.S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.  
 Direct Submission  
 TITLS  
 JOURNAL  
 Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis,  
 Walter Reed Army Institute of Research, 1600 E. Gude Drive,  
 Rockville, MD 20850, USA  
 Location/Qualifiers  
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Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis,  
 Walter Reed Army Institute of Research, 1600 E. Gude Drive,  
 Rockville, MD 20850, USA  
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 receptor expressed on eosinophils, CD4 Th2 lymphocytes,  
 CD8 lymphocytes, microglia, dendritic cells, and  
 monocytes"  
 /codon\_start=1  
 /product="CC chemokine receptor 3"  
 /protein\_id="AAL85631.1"  
 /db\_xref="GI:19171647"  
 /translation="MTSLDTVETFGTTSYDDVGLLCEKADTRALMAQFVPPYLSLV  
 FTVGLLGNVVVMILIKYRRLRIMTNILNLAISD"  
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 Query Match 100.0%; Score 22; DB 9; Length 410;  
 Best Local Similarity 100.0%; Pred. No. 0.033;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CTTGTGCTTATCCGGCAAGAA 22  
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 Db 13 CTTGTGCTTATCCGGCAAGAA 34  
 |||||  
 RESULT 10  
 AF262304  
 LOCUS  
 DEFINITION Homo sapiens clone 7 CC chemokine receptor 3-like mRNA, partial  
 sequence, alternatively spliced.  
 ACCESSION AF262304  
 VERSION AF262304.1 GI:19171650  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 436)  
 Vjrh.S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and  
 Michael,N.L.  
 Transcription Regulation of Human Chemokine Receptor CCR3: Evidence  
 for a Rare TATA-less Promoter Structure Conserved between  
 Drosophila and Humans  
 Genomics 80 (1), 86-95 (2002)  
 22074933  
 MEDLINE  
 12079287  
 PUBLISHED  
 REFERENCE  
 2 (bases 1 to 436)  
 Vjrh.S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.  
 Direct Submission  
 TITLS  
 JOURNAL  
 Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis,  
 Walter Reed Army Institute of Research, 1600 E. Gude Drive,  
 Rockville, MD 20850, USA  
 Location/Qualifiers  
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 1. .436  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
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 /map="3p21"  
 /clone="7"  
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misc_feature 1..436
/notes="CC chemokine receptor 3-like; contains exon 1, exon
3, and intron 3 of the CCR3 gene; alternatively spliced"

ORIGIN
Query Match 100.0%; Score 22; DB 9; Length 436;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGTGCTTATCCGGGCAAGAA 22
|||||
Db 12 CTTGTGCTTATCCGGGCAAGAA 33

RESULT 11
AF224496S1 957 bp DNA linear PRI 02-MAY-2001
LOCUS Homo sapiens CC chemokine receptor 3 (CCR3) gene, exon 1.
ACCESSION AF224496
VERSION AF224496.1 GI:13924485
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 957)
AUTHORS Scotet,E.J.
TITLE CCR3 expression is associated with chromatin remodeling in Th2
cells
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 957)
AUTHORS Scotet,E.J.
TITLE Direct Submission
JOURNAL Submitted (13-JAN-2000) Basel Institute for Immunology, 487
Grenzacherstrasse, Basel CH-4005, Switzerland
FEATURES
source 1..957
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
298..376
/gene="CCR3"
/notes="exon 1"
exon

ORIGIN
Query Match 100.0%; Score 22; DB 9; Length 957;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGTGCTTATCCGGGCAAGAA 22
|||||
Db 310 CTTGTGCTTATCCGGGCAAGAA 331

RESULT 12
AF247360 1453 bp DNA linear PRI 26-JUN-2002
LOCUS Homo sapiens CC chemokine receptor 3 (CCR3) gene, promoter region
and partial sequence.
ACCESSION AF247360
VERSION AF247360.1 GI:19110541
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1453)
AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and
Michael,N.L.
TITLE Transcription Regulation of Human Chemokine Receptor CCR3: Evidence
for a Rare TATA-less Promoter Structure Conserved between
Drosophila and Humans
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Genomics 80 (1), 86-95 (2002)
JOURNAL MEDLINE 22074933
PUBMED 12079287
REFERENCE 2 (bases 1 to 1453)
AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.
TITLE Direct Submission
JOURNAL Submitted (21-MAR-2000) Dept. of Mol. Diag. and Pathogenesis, U.S.
Military HIV Research Program, 1600 E. Gude Drive, Rockville, MD
20850, USA
FEATURES
Location/Qualifiers
source 1..1453
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="3"
/map="3p21; between CCR1 and CCR5"
/clone="A8"
/cell_type="peripheral blood mononuclear cell"
gene 1..>1453
variation 755
/gene="CCR3"
mRNA 822..>1453
/gene="CCR3"
/product="CC chemokine receptor 3"
exon 822..1163
variation 1114
/gene="CCR3"
/replace="g"
ORIGIN
Query Match 100.0%; Score 22; DB 9; Length 1453;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGTGCTTATCCGGGCAAGAA 22
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Db 1097 CTTGTGCTTATCCGGGCAAGAA 1118

RESULT 13
AX513212 2895 bp DNA linear PAT 03-OCT-2002
LOCUS Sequence 11 from Patent WO02062848.
ACCESSION AX513212
VERSION AX513212.1 GI:23504275
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Rothenberg,M.E. and Zimmerman,N.
TITLE Regulation of cc chemokine receptor 3 (ccr3) expression
JOURNAL Patent: WO 02062848-A 11 15-AUG-2002;
CHILDREN'S HOSPITAL MEDICAL CENTER (US)
FEATURES
Location/Qualifiers
source 1..2895
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGTGCTTATCCGGGCAAGAA 22
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Db 1576 CTTGTGCTTATCCGGGCAAGAA 1597
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RESULT 14
LOCUS AF237380S1 2895 bp DNA linear PRI 05-OCT-2000
DEFINITION Homo sapiens CCR3 gene, promoter and exon 1.
ACCESSION AF237380
VERSION AF237380.1 GI:10643652
KEYWORDS
SEGMENT
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE 1 (bases 1 to 2895)
AUTHORS Zimmernann,N., Daugherty,B.L., Kavanaugh,J.L., El-Awar,F.Y.,
Moulton,E.A. and Rotherberg,M.E.
TITLE Analysis of the CC chemokine receptor 3 gene reveals a complex 5'
exon organization, a functional role for untranslated exon 1, and a
broadly active promoter with eosinophil-selective elements
JOURNAL Blood 96 (7), 2346-2354 (2000)
MEDLINE 20458773
PUBMED 11001881
REFERENCE 2 (bases 1 to 2895)
AUTHORS Daugherty,B.L.
TITLE Direct Submission
JOURNAL Submitted (22-FEB-2000) Immunology & Rheumatology, Merck Research
Laboratories, 126 East Lincoln Avenue, Rahway, NJ 07065, USA
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MO)"
promoter
1..1551
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CAAT_signal
33..38
/gene="CCR3"
CAAT_signal
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Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGTGCTTATCGGCAAGAA 22
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Db 1576 CTGTGCTTATCGGCAAGAA 1597
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AC138069 177334 bp DNA linear PRI 19-FEB-2003
LOCUS AC138069
DEFINITION Homo sapiens chromosome 3 clone RP13-54612, complete sequence.
ACCESSION AC138069
VERSION AC138069.3 GI:28416170
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 177334)
AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
Saenphimmachak,C., Buckley,D., Kibukawa,M., Raymond,C. and

```

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Haugen,E.D.
Direct Submission
Unpublished
2 (bases 1 to 177334)
AUTHORS Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.
TITLE Direct Submission
JOURNAL Submitted (12-DEC-2002) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
3 (bases 1 to 177334)
AUTHORS Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.
TITLE Direct Submission
JOURNAL Submitted (10-JAN-2003) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
4 (bases 1 to 177334)
AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
Saenphimmachak,C., Buckley,D., Kibukawa,M., Raymond,C. and
Haugen,E.D.
Direct Submission
Submitted (19-FEB-2003) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
On Feb 19, 2003 this sequence version replaced gi:27573398.
----- Genome Center
Center: University of Washington Genome Center
Center Code: UWGC
Web site: http://www.genome.washington.edu
Contact: uwgctgs@u.washington.edu
----- Project Information
Center project name: chr-3
Center clone name: RP13-54612 (bc0820)
----- Summary Statistics
Sequencing vector: plasmid; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 177210 bases at least Q40
Consensus quality: 177313 bases at least Q30
Consensus quality: 177334 bases at least Q20
Insert size: 177334; sum-of-contigs
Quality coverage: 9.3x in Q20 bases; sum-of-contigs
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Overlapping Sequences:
5': RP11-793E15 (UWGC:bc0564) AC104439, 95469-bp overlap
3': U95626, 42710-bp overlap
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Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the
Genbank flat file format but are available as part
of this entry's ASN.1 file.
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This sequence was finished as follows unless otherwise noted:
all regions were either double-stranded or sequenced with an
alternate chemistry or covered by high quality data (i.e., Phred
quality >= 30); an attempt was made to resolve all sequencing
problems, such as compressions and repeats; all regions were
covered by at least one plasmid subclone or more than one M13
subclone; and the assembly was confirmed by restriction digest.
-----
Sequence Validation:
This sequence has been validated by Multiple Complete Digest
fingerprinting. Comparison of the experimentally derived digest
fragments with sequence-predicted fragments is given below.
The electronically-digested sequence consists of both insert and
vector, in order to accurately represent the entire circular BAC.
Small fragments below a variable cutoff (approximately 400-800 bp)
are not resolved in the fingerprint and hence do not appear
in the table. There are no significant remaining discrepancies
between the experimental and predicted values. Uniquely ordered
fragments are separated by dashed lines.
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HindIII
EcoRI
BglII

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SeqDerMap	FngPrnt	SeqDerMap	FngPrnt	SeqDerMap	FngPrnt
1239	1199	11125	10952	6306	6319
449	<800	2290	2310	2067	2071
510	<800	560	<800	3913	3756
6511	6363	54	<800	2169	2210
5296	5509	1159	1158	910	910
10424	10027	4052	4034	875	883
5046	5119	1846	1829	3716	3756
1196	1199	8334	8273	4502	4523
1397	1392	12882	12573	1967	1945
2597	2624	448	<800	2864	2871
1688	1674	12737	12573	4724	4738
3800	3818	10300	10103	4773	4738
2248	2269	6671	6656	3707	3756
1074	1055	4052	4034	336	<800
7303	7718	1392	1386	79	<800
959	959	4253	4286	4736	4738
551	<800	2791	2834	1889	1945
1074	1055	2647	2682	3696	3756
5688	5759	3423	3409	1569	1539
5183	5363	73	<800	8078	8038
3100	3093	499	<800	1365	1325
921	959	723	<800	289	<800
4350	4244	2763	2834	11047	10790
4931	4857	6594	6656	8848	8963
3907	3818	4503	4468	1914	1945
8001	7718	5154	5136	1336	1325
3804	3818	4730	4713	11485	11341
2355	2376	13628	13324	974	975
862	868	166	<800	2449	2501
1711	1674	9554	9494	373	<800
5672	5759	1398	1386	1003	975
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1905	1854	1479	1503	857	883
7872	7718	1540	1503	1974	1945

1174	1155	520	<800	1707	1631
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221	<800	154	<800	178	<800
1002	1055	5077	5136	2905	2871
201	<800	2156	2190	2500	2501
6717	6864	1075	1089	389	<800
237	<800	162	<800	41	<800
2737	2749	2752	2834	685	<800
3448	3416	1647	1641	2598	2662
3256	3238	7059	7056	248	<800
5801	5759	1547	1503	2152	2210
1512	1497	5163	5136	431	<800
1398	1392	8679	8719	237	<800
8413	8333	2033	2035	3380	3411
6621	6614	886	892	5694	5744
645	<800	---	---	3255	3265
1026	1055	---	---	183	<800
14333	14484	---	---	3128	3144
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Query Match 100.0%; Score 22; DB 9; Length 177334;  
Best Local Similarity 100.0%; Pred. No. 0.016;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTGTCCTTATCCGGCAAGAA 22  
Db 65708 CTTGTCCTTATCCGGCAAGAA 65729

Search completed: August 2, 2004, 19:07:55  
Job time : 495.914 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 2, 2004, 18:06:45 ; Search time 909.207 Seconds  
(without alignments)  
722.573 Million cell updates/sec

Title: US-10-068-067-18  
Perfect score: 22  
Sequence: 1 cttgtgcttaccgggcaagaa 22

Scoring table: OIIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST:\*

- 1: em\_estba:\*
- 2: em\_esthum:\*
- 3: em\_estin:\*
- 4: em\_estmu:\*
- 5: em\_estov:\*
- 6: em\_estpl:\*
- 7: em\_estro:\*
- 8: em\_hic:\*
- 9: gb\_est1:\*
- 10: gb\_est2:\*
- 11: gb\_hic:\*
- 12: gb\_est3:\*
- 13: gb\_est4:\*
- 14: gb\_est5:\*
- 15: em\_estfun:\*
- 16: em\_estom:\*
- 17: em\_gss\_hum:\*
- 18: em\_gss\_inv:\*
- 19: em\_gss\_pin:\*
- 20: em\_gss\_vit:\*
- 21: em\_gss\_fun:\*
- 22: em\_gss\_mam:\*
- 23: em\_gss\_mus:\*
- 24: em\_gss\_pro:\*
- 25: em\_gss\_rod:\*
- 26: em\_gss\_phg:\*
- 27: em\_gss\_vrl:\*
- 28: gb\_gss1:\*
- 29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	100.0	876	12	BI906283
2	18	81.8	584	14	CB390728
3	17	77.3	690	29	CE306183
4	16	72.7	741	28	CC146471

16	72.7	779	29	CG810851	CG810851
15	68.2	191	10	BB482778	BB482778
15	68.2	196	10	BF153648	BF153648
15	68.2	283	12	BI702619	BI702619
15	68.2	327	13	BU097383	BU097383
15	68.2	420	29	CE669510	CE669510
15	68.2	432	9	AV661308	AV661308
15	68.2	432	14	CB818132	CB818132
15	68.2	444	29	AG222515	AG222515
15	68.2	466	14	CA723251	CA723251
15	68.2	476	14	CF040747	CF040747
15	68.2	533	12	BM176155	BM176155
15	68.2	533	29	AG232968	AG232968
15	68.2	537	10	AW221092	AW221092
15	68.2	569	28	BZ460173	BZ460173
15	68.2	571	28	BH829236	BH829236
15	68.2	577	9	AI772554	AI772554
15	68.2	577	12	BG133271	BG133271
15	68.2	593	13	BO915767	BO915767
15	68.2	595	13	BY746429	BY746429
15	68.2	602	10	AW498430	AW498430
15	68.2	622	14	CA215444	CA215444
15	68.2	648	10	AW945046	AW945046
15	68.2	692	28	CC160895	CC160895
15	68.2	717	29	CG952921	CG952921
15	68.2	721	28	BH490719	BH490719
15	68.2	731	28	BZ515527	BZ515527
15	68.2	745	29	CG834018	CG834018
15	68.2	792	29	CG428299	CG428299
15	68.2	907	13	BQ936744	BQ936744
15	68.2	908	29	CG768840	CG768840
15	68.2	1001	10	BE735363	BE735363
15	68.2	1198	10	BF129201	BF129201
14	63.6	120	28	BH642591	BH642591
14	63.6	129	28	BH201059	BH201059
14	63.6	129	28	BH201074	BH201074
14	63.6	158	13	BQ289892	BQ289892
14	63.6	207	13	BQ289891	BQ289891
14	63.6	230	12	BP511882	BP511882
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14	63.6	271	12	BM167016	BM167016

#### ALIGNMENTS

RESULT 1  
BI906283  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

BI906283 876 bp mRNA linear EST 16-OCT-2001  
603063222F1 NIH\_MGC\_118 Homo sapiens cDNA clone IMAGE:5212541 5',  
mRNA sequence.  
BI906283  
BI906283.1 GI:16168946  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 876)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs@mail.nih.gov](mailto:cgabbs@mail.nih.gov)  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.lnl.gov>  
Plate: L1AM11533 row: k column: 06  
High quality sequence stop: 800.

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        non-activated adult donors. Library is oligo-dT primed
        and directionally cloned (EcoRV site is destroyed upon
        cloning). Average insert size 1.7 kb, insert size range
        1.2-3.3 kb. Library is normalized and enriched for
        full-length clones and was constructed by C. Gruber
        (Invitrogen). Research Genetics tracking code 027. Note:
        this is a NIH_MGC Library."

ORIGIN
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  Best Local Similarity 100.0%; Pred. No. 0.028; 0; Indels 0; Gaps 0;
  Matches 22; Conservative 0; Mismatches 0;

QY 1 CTGTGCTTATCCGGGCAAGAA 22
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Db 1 CTGTGCTTATCCGGGCAAGAA 22

RESULT 2
LOCUS CB390728 584 bp mRNA linear EST 15-MAY-2003
DEFINITION OSTE139F9_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION CB390728
VERSION CB390728.1 GI:30732438
KEYWORDS EST.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
REFERENCE 1 (bases 1 to 584)
AUTHORS Reboul,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M.,
Armstrong,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T.,
Hudson,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,
Endress,G.A., Jenna,S., Chevret,E., Papasotiropoulos,V.,
Tollas,P.P., Ptacek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
Doucette-Stamm,L., Hill,D.E. and Vidal,M.
C. elegans ORFeome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
expression
JOURNAL Nat. Genet. (2003) In press
COMMENT Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc.Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david_hilledfci.harvard.edu or
marc_vidal@dfci.harvard.edu
POLYA=NO. Location/Qualifiers
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  source
    Location/Qualifiers

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/notes="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
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subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPCR86"

ORIGIN
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  Best Local Similarity 100.0%; Pred. No. 5.5;
  Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TGTGCTTATCCGGGCAAG 20
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Db 233 TGTGCTTATCCGGGCAAG 250

RESULT 3
LOCUS CB306183 690 bp DNA linear GSS 26-SEP-2003
DEFINITION tigr-gss-dog-17000360539649 Dog Library Canis familiaris genomic,
genomic survey sequence.
ACCESSION CB306183
VERSION CB306183.1 GI:36100308
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
REFERENCE 1 (bases 1 to 690)
AUTHORS Kirkness,E.F., Batina,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
JOURNAL MEDLINE 22875432
PUBMED 14512627
COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: exikrnes@tigr.org
Class: shotgun.
Location/Qualifiers
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  Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTGCTTATCCGGGCAAG 20
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Db 262 GTGCTTATCCGGGCAAG 278

RESULT 4
LOCUS CC146471 741 bp DNA linear GSS 24-JUN-2003
DEFINITION ZMMBBB0008F04.f ZMMBBB Zea mays subsp. mays genomic clone
ACCESSION CC146471
VERSION CC146471.1 GI:30091664
KEYWORDS GSS.
SOURCE Zea mays subsp. mays (maize)

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ORGANISM Zea mays subsp. mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE 1 (bases 1 to 741)  
AUTHORS Yu, Y., Kim, H.R., Hatfield, J., Soderlund, C., Bharti, A.K., Messing, J. and Wang, R.  
TITLE Sequencing of the maize genome  
COMMENT Unpublished (2003)  
Contact: Rod Wing  
Arizona Genomics Institute  
University of Arizona  
Biological Sciences West, 449A, P.O. Box 210088, Tucson, AZ 85721-0088, USA  
Tel: 520 626 3967  
Fax: 520 621 9288  
Email: <http://genome.arizona.edu>  
PCR Primers  
FORWARD: T7  
BACKWARD: M13r  
Plate: 0008 row: F column: 04  
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Class: BAC ends.  
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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 TGCTTATCCGGGCAAG 20  
Db 382 TGCTTATCCGGGCAAG 367  
RESULT 5  
CG810851  
LOCUS  
DEFINITION .FSAL36TR LargeInsertGenomicLibrary Fusarium virguliforme genomic clone KMV3F4, genomic survey sequence.  
ACCESSION CG810851  
VERSION CG810851.1 GI:38264325  
KEYWORDS GSS.  
SOURCE Fusarium virguliforme  
ORGANISM Fusarium virguliforme  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocerales; Nectriaceae; Nectria.  
REFERENCE 1 (bases 1 to 779)  
AUTHORS Meksem, K., Ishihara, H., Koo, H., Shultz, J., Ali, S., Iqbal, J., Lightfoot, D.A. and Town, C.D.  
TITLE End sequencing of BACs from a fingerprint physical map of the causative agent of soybean sudden death syndrome, *Fusarium virguliforme*  
COMMENT Unpublished (2003)  
Contact: Chris Town and K. Meksem  
The Center of Excellence in Soybean Research, Teaching and Outreach, Southern Illinois University at Carbondale and Plant Genomics, The Institute for Genomic Research  
Room 176, Ag Building, Mail Code 4415, Carbondale, IL 62901-4415, USA and 9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 618 453 3103 and 301-838-3523  
Fax: 618 453-7457 and 301-838-0208

Email: meksem@siu.edu; cdtown@tigr.org (URL: <http://Fusariumvirguliform.siu.edu>)  
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Class: BAC ends.  
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1..779  
/organism="Fusarium virguliforme"  
/mol\_type="genomic DNA"  
/cultivar="Monticello"  
/db\_xref="taxon:232082"  
/clone="KMV3F4"  
/clone\_lib="LargeInsertGenomicLibrary"  
/note="Organ: Hyphae; Vector: PINDIGOBAC5; A single spore derived culture was used. Hyphae were grown in an incubator for four days. Nuclei were isolated and embedded in agarose, restriction digested with Hind III. Large size DNA fragments were ligated in vector PINDIGOBAC5 and electro-transformed into DH10B cells."  
ORIGIN  
Query Match 72.7%; Score 16; DB 29; Length 779;  
Best Local Similarity 100.0%; Pred. No. 80;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 GCTTATCCGGGCAAGA 21  
Db 645 GCTTATCCGGGCAAGA 660  
RESULT 6  
BB482778/c  
LOCUS  
DEFINITION BB482778 RIKEN full-length enriched, 13 days embryo lung Mus musculus cDNA clone D430015020 3', similar to U24655 Rattus norvegicus Lnk4 mRNA, mRNA sequence.  
ACCESSION BB482778  
VERSION BB482778.1 GI:9400387  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 191)  
AUTHORS Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, F., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tomimaga, N., Toya, T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.  
RIKEN Mouse ESTs (Konno, H., et al.)  
Unpublished (2000)  
Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: [genome-res@sc.riken.go.jp](mailto:genome-res@sc.riken.go.jp),  
[URL:http://genome.gsc.riken.go.jp/](mailto:URL:http://genome.gsc.riken.go.jp/)  
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Thermosensitization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. *Proc. Natl. Acad. Sci. U.S.A.* 95 (2), 520-524 (1998)  
Itoh, M., Kitsuai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,

Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.  
Automated filtration-based high-throughput plasmid preparation system. *Genome Res.* 9 (5), 463-470 (1999)

Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning. *Methods Enzymol.* 303, 19-44 (1999)  
Please visit our web site (<http://genome.rtc.riken.go.jp/>) for further details.

FEATURES  
source  
Location/Qualifiers  
1..191  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/clone="D430015020"  
/tissue\_type="lung"  
/dev\_stage="13 days embryo"  
/lab\_host="DH10B"  
/clone\_lib="RIKEN full-length enriched, 13 days embryo lung"  
/note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'  
GAGAGAGAGCGCGCGCAACTCGAGTTTCTTTTCTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'  
GAGAGAGATTCGAGTAAATTAATATCCCGCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified paluescript KS(+) after bulk excision from lambda FLC I."

ORIGIN  
Query Match 68.2%; Score 15; DB 10; Length 191;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTGCTTATCGGCGCA 18  
|||||  
Db 37 GTGCTTATCGGCGCA 23

RESULT 7  
BF153648/c  
LOCUS  
DEFINITION  
BF153648 Mature tuber lambda ZAP Solanum tuberosum cDNA 5', mRNA  
sequence.  
ACCESSION  
BF153648  
VERSION  
BF153648.1 GI:11035588  
KEYWORDS  
EST.  
SOURCE  
Solanum tuberosum (potato)  
ORGANISM  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanaceae; Solanum.  
REFERENCE  
1 (bases 1 to 196)  
Crookshanks, M., Emmersen, J., Welinder, K.G. and Nielsen, K.L.  
The potato tuber transcriptome: analysis of 6077 expressed sequence tags  
FEBs Lett. 506 (2), 123-126 (2001)  
JOURNAL  
MEDLINE  
21475600  
PUBMED  
11591384  
COMMENT  
Contact: Karen G. Welinder  
Institut for Biotechnology  
Aalborg Universitet  
Sohngaardsholmsvej 49, 9000 Aalborg, Denmark  
Tel: +45 96358467  
Fax: +45 98141808  
Email: kgw@bio.auc.dk

Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.  
Automated filtration-based high-throughput plasmid preparation system. *Genome Res.* 9 (5), 463-470 (1999)

Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning. *Methods Enzymol.* 303, 19-44 (1999)  
Please visit our web site (<http://genome.rtc.riken.go.jp/>) for further details.

FEATURES  
source  
Location/Qualifiers  
1..196  
/organism="Solanum tuberosum"  
/mol\_type="mRNA"  
/cultivar="Field grown Kuras"  
/db\_xref="taxon:4113"  
/tissue\_type="Tuber"  
/clone\_lib="Mature tuber lambda ZAP"  
/note="Vector: Lambda ZAP"

ORIGIN  
Query Match 68.2%; Score 15; DB 10; Length 196;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGTGCTTATCGCG 15  
|||||  
Db 151 CTTGTGCTTATCGCG 137

RESULT 8  
BF1702619  
LOCUS  
DEFINITION  
BF1702619 283 bp mRNA linear EST 18-SEP-2001  
f38n10.x1 zebrafish adult brain Danio rerio cDNA clone IMAGE:4955779 3' similar to TR:O35274 O35274 SPINOPHILIN.; mRNA sequence.  
ACCESSION  
BF1702619  
VERSION  
BF1702619.1 GI:15665248  
KEYWORDS  
EST.  
SOURCE  
Danio rerio (zebrafish)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.  
REFERENCE  
1 (bases 1 to 283)  
Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Stepcevic, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.  
WashU Zebrafish EST Project 1998  
Unpublished (1998)  
Contact: Stephen L. Johnson  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: zbrfish@watson.wustl.edu  
cDNA Library Preparation: John Ngai. cDNA Library Arrayed by: Matthew Clark. DNA Sequencing by: Washington University Genome Sequencing Center Clone Distribution: Genome Systems, St. Louis, Missouri (web address: [www.genomesystems.com](http://www.genomesystems.com)) (email contact: [info@genomesystems.com](mailto:info@genomesystems.com)) and Research Genetics, Huntsville, Alabama (web address: [www.resgen.com](http://www.resgen.com)) (email contact: [info@resgen.com](mailto:info@resgen.com)) and Ressourcentzentrum Primatendatenbank, Berlin, Germany (web address: [www.rzpd.de](http://www.rzpd.de))  
Trace considered overall poor quality  
Possible reversed clone: polyT not found  
Seq primer: T7 from Gibco  
High quality sequence stop: 1.  
Location/Qualifiers  
1..283  
/organism="Danio rerio"  
/mol\_type="mRNA"  
/db\_xref="taxon:7955"  
/clone="IMAGE:4955779"  
/sex="mixed male and female"  
/tissue\_type="brain"  
/dev\_stage="adult"  
/lab\_host="E. coli DH10B"

```

/clone.lib="zebrafish adult brain"
/note="Vector: pZIPLOX; Site 1: NotI; Site 2: SalI;
Original library was constructed in lambdaZIPLOX. Mass
excision of the cDNA library was performed to yield
pZIPLOX plasmids. Insert check was done in original
library."

ORIGIN
Query Match      68.2%; Score 15; DB 12; Length 283;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TCGTATCCGGGCAA 19
|||||
Db 229 TCGTATCCGGGCAA 243

RESULT 9
BU097383/c
LOCUS tca-1868 tca Trypanosoma carassii cDNA clone 1012 5', mRNA
DEFINITION tca-1868 tca Trypanosoma carassii cDNA clone 1012 5', mRNA
ACCESSION BU097383
VERSION BU097383.1 GI:25125107
KEYWORDS EST.
SOURCE Trypanosoma carassii
ORGANISM Trypanosoma carassii
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
REFERENCE 1 (bases 1 to 327)
AUTHORS Aguero, F., Campo, V., Cremona, L., Jager, A., Di Noia, J.M.,
Overath, P., Sanchez, D.O. and Frasch, A.C.
TITLE Gene discovery in the freshwater fish parasite Trypanosoma
carassii: identification of trans-sialidase-like and mucin-like
genes
JOURNAL Infect. Immun. 70 (12), 7140-7144 (2002)
COMMENT Contact: Sanchez DO
Genomics and Bioinformatics
Instituto de Investigaciones Bioteologicas
Av. Gral Paz S/N, INTI, Edificio 24, B 1650 KNA, San Martin, Buenos
Aires, Argentina
Tel: (54-11) 4580/7255/7
Fax: (54-11) 4752-9639
Email: dsanchez@ib.unsam.edu.ar
Sequences were basecalled with phred and vector was masked with
crossmatch (see http://www.phrap.org). Sequences were then trimmed
from both ends to remove low quality bases and masked vector.
Plate: 10 row: 1 column: 2
Seq primer: T7.
Location/Qualifiers
1..327
/organism="Trypanosoma carassii"
/mol_type="mRNA"
/db_xref="taxon:38249"
/clone="1012"
/dev_stages="blood trypanostigote"
/lab_host="Goldfish (Carassius auratus)"
/clone_lib="tca"
/note="Vector: pSport1; Blood trypanostigotes were
obtained from goldfish and cultured as described (Overath
et al. Parasitol Res (1998) 84:1343) before obtaining total
RNA using TRIzol. cDNA library construction was made from
polyA+ mRNA using a poly-dT oligonucleotide as primer. The
cDNAs were cloned in a oriented manner using a commercial
kit (SuperScript Plasmid System for cDNA Synthesis and
Plasmid Cloning, Life Technologies)."

ORIGIN
Query Match      68.2%; Score 15; DB 13; Length 327;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TCGTATCCGGGCAA 19

```

```

|||||
83 TCGTATCCGGGCAA 69

RESULT 10
CE669510/c
LOCUS tigr-gss-dog-17000329315342 Dog Library Canis familiaris genomic,
DEFINITION genomic survey sequence.
ACCESSION CE669510
VERSION CE669510.1 GI:36988494
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 420)
AUTHORS Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
Venter, O.C.
TITLE The dog genome: survey sequencing and comparative analysis
JOURNAL Science 301 (5641), 1898-1903 (2003)
MEDLINE 22875432
PUBMED 14512627
COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
Location/Qualifiers
1..420
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site 1: BstXI; Libraries were prepared from
peripheral blood"

ORIGIN
Query Match      68.2%; Score 15; DB 29; Length 420;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGCTTATCCGG 15
|||||
Db 93 CTTGCTTATCCGG 79

RESULT 11
AV661308/c
LOCUS AV661308 GLC Homo sapiens cDNA clone GLOCRA09 3', mRNA sequence.
DEFINITION AV661308 GLC Homo sapiens cDNA clone GLOCRA09 3', mRNA sequence.
ACCESSION AV661308
VERSION AV661308.1 GI:9882322
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 432)
AUTHORS Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X.,
Xiao, H., Qu, J., Liu, F., Huang, O., Cheng, Z., Li, N., Du, J., Hu, W.,
Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X.,
Hu, G., Gu, J., Chen, Z. and Han, Z.
TITLE Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
MEDLINE 21625106

```

11752456  
 PUBMED  
 COMMENT  
 Contact: Zequang Han  
 Chinese National Human Genome Center at Shanghai  
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai  
 201203, P. R. China  
 Tel: 86-21-50801919 (ex.45)  
 Fax: 86-21-50801922  
 Email: hanzg@chgc.sh.cn  
 This clone is available at CHGC in Shanghai.

FEATURES  
 source  
 1..432  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="GLCGRA09"  
 /tissue\_type="corresponding non cancerous liver tissue"  
 /dev\_stage="Adult"  
 /lab\_host="SOLR"  
 /clone\_lib="GLC"  
 /note="Vector: pBluescript sk(-); Site\_1: EcoRI; Site\_2: XhoI"

ORIGIN  
 Query Match 58.2%; Score 15; DB 9; Length 432;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CTTATCCGGGCAAGA 21  
 |||||  
 Db 96 CTTATCCGGGCAAGA 82  
 |||||

RESULT 12  
 CB818132/c  
 LOCUS  
 DEFINITION Plumbago zeylanica sperm cell (Svn) cDNA library  
 ACCESSION CB818132  
 VERSION CB818132.1 GI:29950337  
 KEYWORDS EST.  
 SOURCE Plumbago zeylanica  
 ORGANISM Plumbago zeylanica  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Caryophyllales; Plumbaginaceae; Plumbago.  
 1 (bases 1 to 432)  
 Gou.X.P., Yuan.T. and Russell,S.D.  
 mRNAs of Plumbago zeylanica sperm cell populations  
 Unpublished (2003)  
 JOURNAL  
 COMMENT Contact: Russell, Scott  
 Department of Botany and Microbiology  
 University of Oklahoma  
 Norman, OK 73019, USA  
 Tel: 405 325 6234  
 Fax: 405 325 7619  
 Email: srussell@ou.edu  
 Contact Dr. Scott D. Russell regarding clone availability  
 Seq primer: pRIP, 5'TCCGAGATCTGGACGAG3'  
 High quality sequence stop: 426.

FEATURES  
 source  
 1..432  
 /organism="Plumbago zeylanica"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:76149"  
 /clone="a8f10p2"  
 /cell\_type="sperm cell"  
 /dev\_stage="post-anthesis pollen"  
 /lab\_host="E.coli strain XLI-Blue"  
 /clone\_lib="Plumbago zeylanica sperm cell (Svn) cDNA library"  
 /note="Vector: Clontech Triplex2; Sua and Svn sperm cells were isolated and collected in separate pools using a microinjector. cDNA libraries were constructed by oligo dT

priming using the Clontech SMART cDNA Library Construction kit. The cDNAs were directionally cloned into vector Triplex2."

ORIGIN  
 Query Match 68.2%; Score 15; DB 14; Length 432;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTGTGCTTATCCGGG 16  
 |||||  
 Db 200 TTGTGCTTATCCGGG 186  
 |||||

RESULT 13  
 AG222515  
 LOCUS  
 DEFINITION Lotus corniculatus var. japonicus DNA, clone:LjB07e12\_L, genomic survey sequence.  
 ACCESSION AG222515  
 VERSION AG222515.1 GI:26529924  
 KEYWORDS GSS.  
 SOURCE Lotus corniculatus var. japonicus (Lotus japonicus)  
 ORGANISM Lotus corniculatus var. japonicus  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteeae;  
 Lotus.  
 1  
 Sato,S., Nakamura,Y. and Tabata,S.  
 Lotus japonicus BAC End sequences  
 Published Only in Database (2002)  
 REFERENCE 2 (bases 1 to 444)  
 AUTHORS Sato,S.  
 TITLE Direct Submission  
 JOURNAL Submitted (20-NOV-2002) Shusei Sato, Kazusa DNA Research Institute,  
 The First Laboratory for Plant Gene Research; 2-6-7  
 Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan  
 (E-mail:ssato@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/,  
 Tel:81-438-52-3935(ex.2336), Fax:81-438-52-3934)

FEATURES  
 source  
 1..444  
 /organism="Lotus corniculatus var. japonicus"  
 /mol\_type="genomic DNA"  
 /strain="Miyekojima MG-20"  
 /variety="japonicus"  
 /db\_xref="taxon:34305"  
 /clone="LjB07e12 f"  
 /clone\_lib="genomic BAC library"  
 /note="VECTOR:pBelOBAC11-synonym: Lotus japonicus"

ORIGIN  
 Query Match 68.2%; Score 15; DB 29; Length 444;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTGTGCTTATCCGGG 16  
 |||||  
 Db 409 TTGTGCTTATCCGGG 423  
 |||||

RESULT 14  
 CA723251  
 LOCUS  
 DEFINITION wdr1f.pk002.g11 wdr1f Triticum aestivum cDNA clone wdr1f.pk002.g11 end, mRNA sequence.  
 ACCESSION CA723251  
 VERSION CA723251.1 GI:25445044  
 KEYWORDS EST.  
 SOURCE Triticum aestivum (bread wheat)  
 ORGANISM Triticum aestivum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;



REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Pooideae; Triticeae; Triticum.  
1. (bases 1 to 466)  
Tingey,S.V., Powell,W., Walters,P., Dolan,M., Hainey,C., Yuan,Z.,  
Miao,G., Caraher,N. and Hanafey,M.K.  
DuPont Wheat cDNA Sequence  
Unpublished (2002)  
Contact: Scott V. Tingey  
Crop Genetics  
E. I. DuPont de Nemours and Company  
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA  
Tel: 302-631-2602  
Fax: 302-631-2607  
Email: Scott.V.Tingey@USA.dupont.com  
Seq primer: M13.

FEATURES  
source  
location/Qualifiers

1..466  
/organism="Triticum aestivum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4565"  
/clone="wdr1f.pk002.g11"  
/tissue\_type="root"  
/lab\_host="DH10B"  
/clone\_lib="wdr1f"  
/note="Vector: pluescript SK+; Site 1: EcoRI; Site 2:  
xhoI; Wheat (Triticum aestivum) developing root (full  
length)"

## ORIGIN

Query Match 68.2%; Score 15; DB 14; Length 466;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TTATCCGGGCAAGAA 22  
|||||  
Db 329 TTATCCGGGCAAGAA 343

RESULT 15  
CF040747  
LOCUS 476 bp mRNA linear EST 17-JUL-2003  
DEFINITION QC117h09.YG QCI Zea mays cDNA clone QC117h09, mRNA sequence.  
ACCESSION CF040747  
VERSION CF040747.1 GI:32935935  
KEYWORDS EST.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 476)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Genoplante.  
Genoplante, a major partnership french program in plant genomics  
Unpublished (2003)  
Contact: Genoplante  
Genoplante  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplante' (<http://www.genoplante.com>  
and <http://genoplante-info.inbioigen.fr>).

FEATURES  
source  
location/Qualifiers

1..476  
/organism="Zea mays"  
/mol\_type="mRNA"  
/cultivar="F2"  
/db\_xref="taxon:4577"  
/clone="QC117h09"  
/tissue\_type="embryo"  
/clone\_lib="QCI"

## ORIGIN

Query Match 68.2%; Score 15; DB 14; Length 476;

Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TTGTGCTTATCCGGG 16  
|||||  
Db 23 TTGTGCTTATCCGGG 37

Search completed: August 2, 2004, 20:28:05  
Job time : 913.207 secs

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OM nucleic - nucleic search, using sw model

Run on: August 2, 2004, 17:27:15 ; Search time 470.509 seconds  
(without alignments)  
1934.510 Million cell updates/sec

Title: US-10-068-067-19

Perfect score: 21  
Sequence: 1 gcaagaacttctgaaataca 21

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

Database :

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1: gb\_ba.\*

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9: gb\_pr.\*

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20: em\_nu.\*

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33: em\_htg\_mus.\*

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35: em\_htg\_rod.\*

36: em\_htg\_man.\*

37: em\_htg\_vrt.\*

38: em\_sy.\*

39: em\_htgo\_hum.\*

40: em\_htgo\_mus.\*

41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	21	100.0	21	6	AX513220	AX513220 Sequence
2	21	100.0	21	6	AX513225	AX513225 Sequence
3	21	100.0	51	6	AX513217	AX513217 Sequence
4	21	100.0	51	6	AX513222	AX513222 Sequence
5	21	100.0	212	9	AF262303	AF262303 Homo sapi
6	21	100.0	260	9	AF224495	AF224495 Homo sapi
7	21	100.0	348	9	AF262299	AF262299 Homo sapi
8	21	100.0	406	9	AF262301	AF262301 Homo sapi
9	21	100.0	410	9	AF262302	AF262302 Homo sapi
10	21	100.0	436	9	AF262304	AF262304 Homo sapi
11	21	100.0	957	9	AF224496	AF224496 Homo sapi
12	21	100.0	1193	6	AR300122	AR300122 Sequence
13	21	100.0	1193	6	BD082061	BD082061 G-protein
14	21	100.0	1453	9	AF247360	AF247360 Homo sapi
15	21	100.0	2895	6	AX513212	AX513212 Sequence
16	21	100.0	2895	9	AF237380S1	AF237380 Homo sapi
17	21	100.0	177334	9	AC138069	AC138069 Homo sapi
18	21	100.0	197279	9	AC104439	AC104439 Homo sapi
19	21	100.0	220965	2	HS312688	AJ312688 Homo sapi
20	18	85.7	1454	9	AF247359	AF247359 Homo sapi
21	17	81.0	6991	3	PFARHPR	L27838 Plasmodium
22	17	81.0	8241	3	AF323443	AF323443 Plasmodiu
23	17	81.0	8256	3	AF323442	AF323442 Plasmodiu
24	17	81.0	95556	9	HSJ73H14	AL080272 Human DNA
25	17	81.0	95613	2	AC020389	AC020389 Drosophil
C 26	17	81.0	121524	8	AF041468	AF041468 Guillard
C 27	17	81.0	128574	8	OSJN00199	AL663002 Oryza sat
C 28	17	81.0	155840	2	AC006495	AC006495 Drosophil
C 29	17	81.0	174518	2	AC141658	AC141658 Homo sapi
C 30	17	81.0	199044	3	AC009394	AC009394 Drosophil
C 31	17	81.0	224890	3	AE003721	AE003721 Drosophil
C 32	16	76.2	1301	8	AK103163	AK103163 Oryza sat
33	16	76.2	2145	8	AF180024	AF180024 Huperzia
34	16	76.2	3187	8	CHCRPS13	X05847 C.reinhardt
C 35	16	76.2	10305	1	AE002502	AE002502 Neisseria
C 36	16	76.2	10707	1	AE002316	AE002316 Chlamydia
C 37	16	76.2	10733	1	AE009750	AE009750 Pyrobacul
C 38	16	76.2	116673	2	AC141923	AC141923 Medicago
C 39	16	76.2	141111	8	AF002461	AF002461 Oryza sat
C 40	16	76.2	155085	8	AP005693	AP005693 Oryza sat
C 41	16	76.2	155327	9	AC138761	AC138761 Homo sapi
C 42	16	76.2	198756	9	AC087575	AC087575 Homo sapi
C 43	16	76.2	199035	2	AC022263	AC022263 Homo sapi
C 44	16	76.2	307343	1	AE016998	AE016998 Bacillus
C 45	16	76.2	349980	6	AX044033	AX044033 Sequence

ALIGNMENTS

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LOCUS	Sequence 19 from Patent WO02062848.					
DEFINITION	AX513220					
ACCESSION	AX513220					
VERSION	AX513220.1	GI:23504283				
KEYWORDS	Homo sapiens (human)					
SOURCE	Homo sapiens					
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE 1	Rothenberg, M.E. and Zimmerman, N.					
AUTHORS	Regulation of cc chemokine receptor 3 (ccr3) expression					
TITLE	Patent: WO 02062848-A 19 15-AUG-2002;					
JOURNAL						

## CHILDREN'S HOSPITAL MEDICAL CENTER (US)

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QY 1 GCAAGAACTTATCGAATAACA 21  
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 Db 1 GCAAGAACTTATCGAATAACA 21

## RESULT 2

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 LOCUS AX513225 21 bp RNA linear PAT 03-OCT-2002  
 DEFINITION Sequence 24 from Patent WO02062848.  
 ACCESSION AX513225  
 VERSION AX513225.1 GI:23504288

KEYWORDS  
 SOURCE Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 Rothenberg, M.E. and Zimmerman, N.  
 AUTHORS Regulation of cc chemokine receptor 3 (ccr3) expression  
 TITLE Patent: WO 02062848-A 24 15-AUG-2002;  
 JOURNAL CHILDREN'S HOSPITAL MEDICAL CENTER (US)

## FEATURES

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 Matches 21; Conservative 0; Mismatches 0;

QY 1 GCAAGAACTTATCGAATAACA 21  
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 Db 1 GCAAGAACTTATCGAATAACA 21

## RESULT 3

AX513217  
 LOCUS AX513217 51 bp DNA linear PAT 03-OCT-2002  
 DEFINITION Sequence 16 from Patent WO02062848.  
 ACCESSION AX513217  
 VERSION AX513217.1 GI:23504280

KEYWORDS  
 SOURCE Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 Rothenberg, M.E. and Zimmerman, N.  
 AUTHORS Regulation of cc chemokine receptor 3 (ccr3) expression  
 TITLE Patent: WO 02062848-A 16 15-AUG-2002;  
 JOURNAL CHILDREN'S HOSPITAL MEDICAL CENTER (US)

## FEATURES

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Best Local Similarity 100.0%; Pred. No. 0.046;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGAACTTATCGAATAACA 21  
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 Db 31 GCAAGAACTTATCGAATAACA 51

## RESULT 4

AX513222  
 LOCUS AX513222 51 bp RNA linear PAT 03-OCT-2002  
 DEFINITION Sequence 21 from Patent WO02062848.  
 ACCESSION AX513222  
 VERSION AX513222.1 GI:23504285

KEYWORDS

SOURCE Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 Rothenberg, M.E. and Zimmerman, N.  
 AUTHORS Regulation of cc chemokine receptor 3 (ccr3) expression  
 TITLE Patent: WO 02062848-A 21 15-AUG-2002;  
 JOURNAL CHILDREN'S HOSPITAL MEDICAL CENTER (US)

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 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGAACTTATCGAATAACA 21  
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 Db 31 GCAAGAACTTATCGAATAACA 51

## RESULT 5

AF262303  
 LOCUS AF262303 212 bp mRNA linear PRI 26-JUN-2002  
 DEFINITION Homo sapiens clone 6 CC chemokine receptor 3 (CCR3) mRNA, partial

CCS.

ACCESSION AF262303

VERSION AF262303.1 GI:19171648

KEYWORDS

SOURCE Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 212)

## AUTHORS

Vijh, S., Dayhoff, D.E., Wang, C.E., Imam, Z., Ehrenberg, P.K. and Michael, N.L.

## TITLE

Transcription Regulation of Human Chemokine Receptor CCR3: Evidence

for a Rare TATA-less Promoter Structure Conserved between

Drosophila and Humans

JOURNAL Genomics 80 (1), 86-95 (2002)

MEDLINE 22074933

PUBMED 12079287

REFERENCE 2 (bases 1 to 212)

AUTHORS Vijh, S., Dayhoff, D.E., Wang, C.E., Ehrenberg, P.K. and Michael, N.L.

TITLE Direct Submission

JOURNAL Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis,

Walter Reed Army Institute of Research, 1600 E. Gude Drive,

Rockville, MD 20850, USA

FEATURES

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Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGAACTTATCGAATACA 21
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Db 27 GCAAGAACTTATCGAATACA 47
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RESULT 6
AF224495 260 bp mRNA linear PRI 02-MAY-2001
LOCUS Homo sapiens CC chemokine receptor 3 (CCR3) mRNA, partial cds.
DEFINITION Homo sapiens CC chemokine receptor 3 (CCR3) mRNA, partial cds.
ACCESSION AF224495
VERSION AF224495.1 GI:13924481
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 260)
AUTHORS Scotet,E.J.
TITLE CCR3 expression is associated with chromatin remodeling in Th2
cells
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 260)
AUTHORS Scotet,E.J.
TITLE Direct Submission
JOURNAL Submitted (13-JAN-2000) Basel Institute for Immunology, 487
Grenzacherstrasse, Basel CH-4005, Switzerland
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91..>260
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/db_xref="GI:13924482"
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FTVGLGNVVVV"

gene
CDS

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Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGAACTTATCGAATACA 21
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Db 28 GCAAGAACTTATCGAATACA 48
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RESULT 7
AF262299 348 bp mRNA linear PRI 26-JUN-2002
LOCUS Homo sapiens clone 1 CC chemokine receptor 3 (CCR3) mRNA, partial
DEFINITION cds.
ACCESSION AF262299
VERSION AF262299.1 GI:19171640
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 348)
AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.B., Imam,Z., Ehrenberg,P.K. and
Michael,N.I.
TITLE Transcription Regulation of Human Chemokine Receptor CCR3: Evidence
for a Rare TATA-less Promoter Structure Conserved between
Drosophila and Humans
Genomics 80 (1), 86-95 (2002)
JOURNAL MEDLINE
PUBMED 12074933
REFERENCE 2 (bases 1 to 348)
AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.B., Ehrenberg,P.K. and Michael,N.I.
TITLE Direct Submission
JOURNAL Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis,
Walter Reed Army Institute of Research, 1600 E. Gude Drive,
Rockville, MD 20850, USA
FEATURES
Location/Qualifiers
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/db_xref="GI:19171641"
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gene
CDS

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Db 57 GCAAGAACTTATCGAATACA 77
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RESULT 8
AF262301 406 bp mRNA linear PRI 26-JUN-2002
LOCUS Homo sapiens clone 4 CC chemokine receptor 3 (CCR3) mRNA, partial
DEFINITION cds.
ACCESSION AF262301
VERSION AF262301.1 GI:19171644
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

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REFERENCE 1 (bases 1 to 406)  
 AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and Michael,N.L.  
 TITLE Transcription Regulation of Human Chemokine Receptor CCR3: Evidence for a Rare TATA-less Promoter Structure Conserved between Drosophila and Humans  
 JOURNAL Genomics 80 (1), 86-95 (2002)  
 MEDLINE 22074933  
 PUBMED 12079287  
 REFERENCE 2 (bases 1 to 406)  
 AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.  
 TITLE Direct Submission  
 JOURNAL Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis, Walter Reed Army Institute of Research, 1600 E. Gude Drive, Rockville, MD 20850, USA

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 Best Local Similarity 100.0%; Pred. No. 0.042;  
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QY 1 GCAAGAACTTATCGAATACA 21  
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 Db 28 GCAAGAACTTATCGAATACA 48

RESULT 9  
 AF262302  
 LOCUS 410 bp mRNA linear PRI 26-JUN-2002  
 DEFINITION Homo sapiens clone 5 CC chemokine receptor 3 (CCR3) mRNA, partial cds.  
 ACCESSION AF262302  
 VERSION AF262302.1 GI:19171646  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 410)  
 REFERENCE  
 AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and Michael,N.L.  
 TITLE Transcription Regulation of Human Chemokine Receptor CCR3: Evidence for a Rare TATA-less Promoter Structure Conserved between Drosophila and Humans  
 JOURNAL Genomics 80 (1), 86-95 (2002)  
 MEDLINE 22074933  
 PUBMED 12079287  
 REFERENCE 2 (bases 1 to 410)  
 AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.  
 TITLE Direct Submission

JOURNAL Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis, Walter Reed Army Institute of Research, 1600 E. Gude Drive, Rockville, MD 20850, USA

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 /product="CC chemokine receptor 3"  
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 Best Local Similarity 100.0%; Pred. No. 0.042;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 28 GCAAGAACTTATCGAATACA 48

RESULT 10  
 AF262304  
 LOCUS 436 bp mRNA linear PRI 26-JUN-2002  
 DEFINITION Homo sapiens clone 7 CC chemokine receptor 3-like mRNA, partial sequence, alternatively spliced.  
 ACCESSION AF262304  
 VERSION AF262304.1 GI:19171650  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 436)  
 REFERENCE  
 AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and Michael,N.L.  
 TITLE Transcription Regulation of Human Chemokine Receptor CCR3: Evidence for a Rare TATA-less Promoter Structure Conserved between Drosophila and Humans  
 JOURNAL Genomics 80 (1), 86-95 (2002)  
 MEDLINE 22074933  
 PUBMED 12079287  
 REFERENCE 2 (bases 1 to 436)  
 AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.  
 TITLE Direct Submission  
 JOURNAL Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis, Walter Reed Army Institute of Research, 1600 E. Gude Drive, Rockville, MD 20850, USA

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Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGAACTTATCGAAATACA 21
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Db 27 GCAAGAACTTATCGAAATACA 47

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LOCUS AF224496S1 957 bp DNA linear PRI 02-MAY-2001
DEFINITION Homo sapiens CC chemokine receptor 3 (CCR3) gene, exon 1.
ACCESSION AF224496
VERSION AF224496.1 GI:13924485
KEYWORDS
SEGMENT i of 2
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 957)
AUTHORS Scotet,E.J.
TITLE CCR3 expression is associated with chromatin remodeling in Th2
  cells
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 957)
AUTHORS Scotet,E.J.
TITLE Direct Submission
JOURNAL Submitted (13-JAN-2000) Basel Institute for Immunology, 487
  Grenzachstrasse, Basel CH-4005, Switzerland
FEATURES
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    /db_xref="taxon:9606"
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    /note="exon 1"

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Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 325 GCAAGAACTTATCGAAATACA 345

RESULT 12
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LOCUS AR300122
DEFINITION Sequence 3 from patent US 6537764.
ACCESSION AR300122
VERSION AR300122.1 GI:31687431
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1193)
AUTHORS Gerard,C.J., Gerard,N.P., Mackay,C.R., Ponath,P.D., Post,T.W. and
  Qin,S
TITLE Method of identifying inhibitors of C-C chemokine receptor 3
JOURNAL Patent: US 6537764-A 3 25-MAR-2003;
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGAACTTATCGAAATACA 21
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Db 15 GCAAGAACTTATCGAAATACA 35

RESULT 13
LOCUS BD082061 1193 bp DNA linear PAT 27-AUG-2002
DEFINITION G-protein coupled receptor antagonists.
ACCESSION BD082061
VERSION BD082061.1 GI:22627671
KEYWORDS JP 2001524068-A/2.
SOURCE Zea mays
ORGANISM Zea mays
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
  clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 1193)
AUTHORS Mackay,C.R. and Ponath,P.D.
TITLE G-protein coupled receptor antagonists
JOURNAL Patent: JP 2001524068-A 2 27-NOV-2001;
  LEUKOSITE INC
COMMENT PN JP 2001524068-A/2
  PD 27-NOV-2001
  PF 24-SEP-1997 JP 1998516642
  PR 30-SEP-1996 US 08/720565
  PI CHARLES R MACKAY, PAUL D PONATH
  PC C07K16/18;C07K16/28;A61K39/395
  CC Strandedness: Double;
  CC Topology: Linear;
  FH Key Location/Qualifiers
  FT CDS Location/Qualifiers
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      /organism="Zea mays"
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      /db_xref="taxon:4577"

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Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGAACTTATCGAAATACA 21
  |||||
Db 15 GCAAGAACTTATCGAAATACA 35

RESULT 14
AF247360 1453 bp DNA linear PRI 26-JUN-2002
LOCUS AF247360
DEFINITION Homo sapiens CC chemokine receptor 3 (CCR3) gene, promoter region
  and partial sequence.
ACCESSION AF247360
VERSION AF247360.1 GI:19110541
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1453)
AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and
  Michael,N.I.
TITLE Transcription Regulation of Human Chemokine Receptor CCR3: Evidence
  for a Rare TATA-less Promoter Structure Conserved between
  Drosophila and Humans

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Search completed: August 2, 2004, 19:07:57  
Job time : 472.509 secs

JOURNAL Genomics 80 (1), 86-95 (2002)  
MEDLINE 22074933  
PUBMED 12079287  
REFERENCE 2 (bases 1 to 1453)  
AUTHORS Vijh, S., Dayhoff, D.E., Wang, C.E., Ehrenberg, P.K. and Michael, N.L.  
TITLE Direct Submission  
JOURNAL Submitted (21-MAR-2000) Dept. of Mol. Diag. and Pathogenesis, U.S.  
Military HIV Research Program, 1600 E. Gude Drive, Rockville, MD  
20850, USA

FEATURES  
source Location/Qualifiers  
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/chromosome="3"  
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/clone="A8"  
/cell\_type="peripheral blood mononuclear cell"  
1..1453  
/gene="CCR3"  
755  
variation  
/gene="CCR3"  
/replace="t"  
822..1453  
mRNA  
/gene="CCR3"  
/product="CC chemokine receptor 3"  
822..1163  
exon  
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1114  
variation  
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## ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.04; Mismatches 0; Indels 0; Gaps 0;  
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|||||  
DB 1112 GCAAGAACTTATCGAATACA 1132

RESULT 15  
AX513212 2895 bp DNA linear PAT 03-OCT-2002  
LOCUS  
DEFINITION Sequence 11 from Patent WO02062848.  
ACCESSION AX513212  
VERSION AX513212.1 GI:23504275  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
REFERENCE  
AUTHORS Rothenberg, M.E. and Zimmerman, N.  
TITLE Regulation of cc chemokine receptor 3 (ccr3) expression  
JOURNAL Patent: WO 02062848-A 11 15-AUG-2002;  
CHILDREN'S HOSPITAL MEDICAL CENTER (US)  
FEATURES  
source Location/Qualifiers  
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/db\_xref="taxon:9606"

## ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.039; Mismatches 0; Indels 0; Gaps 0;  
Matches 21; Conservative 0;

QY 1 GCAAGAACTTATCGAATACA 21  
|||||  
DB 1591 GCAAGAACTTATCGAATACA 1611



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 2, 2004, 16:56:38 ; Search time 101.379 Seconds

(without alignments)  
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Title: US-10-068-067-19

Perfect score: 21

Sequence: 1 gcaagaacttatcgaaataca 21

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 337863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

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- 3: Geneseqn2000s.\*
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- 5: Geneseqn2001bs.\*
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- 7: Geneseqn2003as.\*
- 8: Geneseqn2003bs.\*
- 9: Geneseqn2003cs.\*
- 10: Geneseqn2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	21	100.0	21	6	ABQ78517 Nucleotid
3	21	100.0	51	6	ABQ78514 Nucleotid
4	21	100.0	51	6	ABQ78519 Nucleotid
5	21	100.0	1193	2	AAAT31335 CC-chemok
6	21	100.0	1193	2	AAV07403 Human C-C
7	21	100.0	2895	6	ABQ78513 Nucleotid
8	17	81.0	3140	4	ABL12512 Drosophil
9	17	81.0	4400	4	ABL12414 Drosophil
10	16	76.2	5532	3	AAAB1538
11	16	76.2	110000	3	AAAB1489
12	16	76.2	349980	3	AAAF21611
13	15	71.4	537	3	AAC94557
14	15	71.4	864	7	ACF70596
15	15	71.4	1056	4	ABL2529 Drosophil
16	15	71.4	1230	6	ABN67605 Streptoco
17	15	71.4	1674	6	ABZ12860 Arabidops
18	15	71.4	1868	3	AAC43679
19	15	71.4	3739	4	ABL2528 Drosophil
20	15	71.4	8920	2	AAQ62924
21	15	71.4	5561	6	ABN71527
22	15	71.4	110000	3	AAAF2305
23	15	71.4	110000	7	ACF67367

C	24	15	71.4	110000	7	ACF65388	11	Continuation (12 o
C	25	15	71.4	265118	5	AAH41227		AAH41227 Pyrococ
C	26	14	66.7	237	7	ACF70657		ACF70657 Phototab
C	27	14	66.7	538	2	AAAX30895		AAAX30895 Streptoco
C	28	14	66.7	564	7	ACA29622		ACA29622 Prokaryot
C	29	14	66.7	647	6	ABQ65988		ABQ65988 Arabidops
C	30	14	66.7	669	6	ABN69167		ABN69167 Streptoco
C	31	14	66.7	669	6	ABN69168		ABN69168 Streptoco
C	32	14	66.7	672	7	ACA50681		ACA50681 Prokaryot
C	33	14	66.7	893	6	ABQ76400		ABQ76400 S. cerevi
C	34	14	66.7	898	4	AAAS7071		AAAS7071 C. tracho
C	35	14	66.7	898	9	ADD42725		ADD42725 Chlamydia
C	36	14	66.7	1338	7	ACA24565		ACA24565 Prokaryot
C	37	14	66.7	1374	3	AAAV70165		AAAV70165 Plasmodiu
C	38	14	66.7	1545	3	AAFI2974		AAFI2974 Aspergill
C	39	14	66.7	1548	7	ABX06868		ABX06868 S. pneumo
C	40	14	66.7	1566	7	ACA49927		ACA49927 Prokaryot
C	41	14	66.7	2177	2	AAZ10370		AAZ10370 DNA encod
C	42	14	66.7	2354	4	AAAS7070		AAAS7070 C. tracho
C	43	14	66.7	2354	9	ADD42724		ADD42724 Chlamydia
C	44	14	66.7	2424	4	AAAD06040		AAAD06040 Yeast YAK
C	45	14	66.7	2771	7	AAAD53418		AAAD53418 Aspergill

#### ALIGNMENTS

#### RESULT 1

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ID ABQ78587 standard; RNA; 21 BP.  
XX  
AC ABQ78587;  
XX  
DT 25-NOV-2002 (first entry)  
XX  
DE Nucleotide sequence of a regulatory sequence for human CCR3.  
XX  
KW Human; CC chemokine receptor 3; CCR3; allergic disorder; probe;  
KW inflammatory disorder; eosinophil; hypersensitivity; leukemia;  
KW infectious disorder; HIV; respiratory syncytial virus infection; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200262848-A2.  
XX  
PD 15-AUG-2002.  
XX  
PF 06-FEB-2002; 2002WO-US003442.  
XX  
PR 07-FEB-2001; 2001US-0267073P.  
PR 05-FEB-2002; 2002US-00068067.  
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
XX  
PI Rothenberg ME, Zimmerman N;  
XX  
DR WPI; 2002-657524/70.  
XX  
XX New CC chemokine receptor 3 (CCR3) regulatory site in an untranslated  
PT exon 1, exon 2, exon 3 or promoter of a human CCR3 gene or mRNA capable  
PT of binding to regulatory elements, useful for preventing e.g. allergic  
PT inflammatory reactions.  
XX  
XX Claim 8; Page 56; 56pp; English.  
PS  
CC The present sequence represents a probe for the human CC chemokine  
CC receptor 3 (CCR3) gene. The probe is a regulatory sequence for CCR3. CCR3  
CC is expressed on cells involved in allergic and/or inflammatory disorders.  
CC The gene comprises 4 exons, with the coding region present on exon 4. The  
CC specification describes methods of regulating the expression of CCR3. The  
CC regulatory site is derived from an untranslated exon 1, exon 2, exon 3 or  
CC promoter of a human CCR3 gene. Regulating the expression of the chemokine  
CC receptor CCR3 is useful for preventing or treating disorders involving

CC eosinophils, such as allergic inflammatory and hypersensitivity  
 CC reactions, certain types of leukemia, and certain infectious disorders  
 CC involving CCR3, e.g. HIV or respiratory syncytial virus infection.  
 CC Expression and modulation of CCR3 is a useful tool in assessing  
 CC eosinophil targeting and in regulating eosinophil-mediated reactions and  
 CC diseases  
 XX  
 SQ Sequence 21 BP; 10 A; 4 C; 3 G; 0 T; 4 U; 0 Other;

Query Match 100.0%; Score 21; DB 6; Length 21;  
 Best Local Similarity 81.0%; Pred. No. 0.025;  
 Matches 17; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2  
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 ID ABQ78517 standard; DNA; 21 BP.  
 XX  
 AC ABQ78517;  
 XX  
 DT 25-NOV-2002 (first entry)  
 XX  
 DE Nucleotide sequence of a regulatory sequence for human CCR3.  
 XX  
 KW Human; CC chemokine receptor 3; CCR3; allergic disorder; probe;  
 KW inflammatory disorder; eosinophil; hypersensitivity; leukemia;  
 KW infectious disorder; HIV; respiratory syncytial virus infection; ss.  
 XX  
 OS Homo sapiens.

XX  
 PN WO200262848-A2.  
 XX  
 PD 15-AUG-2002.  
 XX

PF 06-FEB-2002; 2002WO-US003442.

PR 07-FEB-2001; 2001US-0267073P.

PR 05-FEB-2002; 2002US-00068067.

XX (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.

XX Rothenberg ME, Zimmermann N;

XX WPI; 2002-657524/70.

XX New CC chemokine receptor 3 (CCR3) regulatory site in an untranslated  
 XX exon 1, exon 2, exon 3 or promoter of a human CCR3 gene or mRNA capable  
 XX of binding to regulatory elements, useful for preventing e.g. allergic  
 XX inflammatory reactions.

XX Claim 6; Page 54; 56pp; English.

XX The present sequence represents a probe for the human CC chemokine  
 XX receptor 3 (CCR3) gene. The probe is a regulatory sequence for CCR3. CCR3  
 XX is expressed on cells involved in allergic and/or inflammatory disorders.  
 XX The gene comprises 4 exons, with the coding region present on exon 4. The  
 XX specification describes methods of regulating the expression of CCR3. The  
 XX regulatory site is derived from an untranslated exon 1, exon 2, exon 3 or  
 XX promoter of a human CCR3 gene. Regulating the expression of the chemokine  
 XX receptor CCR3 is useful for preventing or treating disorders involving  
 XX eosinophils, such as allergic inflammatory and hypersensitivity  
 XX reactions, certain types of leukemia, and certain infectious disorders  
 XX involving CCR3, e.g. HIV or respiratory syncytial virus infection.  
 XX Expression and modulation of CCR3 is a useful tool in assessing  
 XX eosinophil targeting and in regulating eosinophil-mediated reactions and  
 XX diseases

XX Sequence 21 BP; 10 A; 4 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 6; Length 21;  
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 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 GCAAGAACTTATCGAATAACA 21

RESULT 3  
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 ID ABQ78514 standard; DNA; 51 BP.  
 XX  
 AC ABQ78514;  
 XX  
 DT 25-NOV-2002 (first entry)  
 XX  
 DE Nucleotide sequence of a regulatory sequence for human CCR3.

XX Human; CC chemokine receptor 3; CCR3; allergic disorder; probe;  
 XX inflammatory disorder; eosinophil; hypersensitivity; leukemia;  
 XX infectious disorder; HIV; respiratory syncytial virus infection; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX misc\_binding 24..27

XX /tag= a

XX /note= "transcription factor binding site for GATA"

XX misc\_binding 40..43

XX /tag= b

XX /note= "transcription factor binding site for GATA"

XX WO200262848-A2.

XX 15-AUG-2002.

XX 06-FEB-2002; 2002WO-US003442.

XX 07-FEB-2001; 2001US-0267073P.

XX 05-FEB-2002; 2002US-00068067.

XX (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.

XX Rothenberg ME, Zimmermann N;

XX WPI; 2002-657524/70.

XX New CC chemokine receptor 3 (CCR3) regulatory site in an untranslated  
 XX exon 1, exon 2, exon 3 or promoter of a human CCR3 gene or mRNA capable  
 XX of binding to regulatory elements, useful for preventing e.g. allergic  
 XX inflammatory reactions.

XX Claim 2; Page 25; 56pp; English.

XX The present sequence represents a probe for the human CC chemokine  
 XX receptor 3 (CCR3) gene. The probe comprises -10 to +60 of exon 1 of CCR3,  
 XX and is a regulatory sequence for CCR3. CCR3 is expressed on cells  
 XX involved in allergic and/or inflammatory disorders. The gene comprises 4  
 XX exons, with the coding region present on exon 4. The specification  
 XX describes methods of regulating the expression of CCR3. The regulatory  
 XX site is derived from an untranslated exon 1, exon 2, exon 3 or promoter  
 XX of a human CCR3 gene. Regulating the expression of the chemokine receptor  
 XX CCR3 is useful for preventing or treating disorders involving  
 XX eosinophils, such as allergic inflammatory and hypersensitivity  
 XX reactions, certain types of leukemia, and certain infectious disorders  
 XX involving CCR3, e.g. HIV or respiratory syncytial virus infection.  
 XX Expression and modulation of CCR3 is a useful tool in assessing  
 XX eosinophil targeting and in regulating eosinophil-mediated reactions and  
 XX diseases

XX Sequence 51 BP; 13 A; 12 C; 11 G; 15 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 6; Length 51;  
Best Local Similarity 100.0%; Pred. No. 0.024;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGAACTTATCGAAATACA 21  
DB 31 GCAAGAACTTATCGAAATACA 51

## RESULT 4

ABQ78519  
ID ABQ78519 standard; RNA; 51 BP.

XX AC ABQ78519;

XX DT 25-NOV-2002 (first entry)

XX DE Nucleotide sequence of a regulatory sequence for human CCR3.

XX KW Human; CC chemokine receptor 3; CCR3; allergic disorder; probe;  
XX KW inflammatory disorder; eosinophil; hypersensitivity; leukemia;  
XX KW infectious disorder; HIV; respiratory syncytial virus infection; ss.

XX OS Homo sapiens.

XX PN WO200262848-A2.

XX PD 15-AUG-2002.

XX PF 06-FEB-2002; 2002WO-US003442.

XX PR 07-FEB-2001; 2001US-0267073P.

XX PR 05-FEB-2002; 2002US-00068067.

XX PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.

XX PI Rothenberg ME, Zimmerman N;

XX DR WPI; 2002-657524/70.

XX PT New CC chemokine receptor 3 (CCR3) regulatory site in an untranslated  
XX PT exon 1, exon 2, exon 3 or promoter of a human CCR3 gene or mRNA capable  
XX PT of binding to regulatory elements, useful for preventing e.g. allergic  
XX PT inflammatory reactions.

XX PS Claim 7; Page 56; 56pp; English.

XX CC The present sequence represents a probe for the human CC chemokine  
XX CC receptor 3 (CCR3) gene. The probe is a regulatory sequence for CCR3. CCR3  
XX CC is expressed on cells involved in allergic and/or inflammatory disorders.  
XX CC The gene comprises 4 exons, with the coding region present on exon 4. The  
XX CC specification describes methods of regulating the expression of CCR3. The  
XX CC regulatory site is derived from an untranslated exon 1, exon 2, exon 3 or  
XX CC promoter of a human CCR3 gene. Regulating the expression of the chemokine  
XX CC receptor CCR3 is useful for preventing or treating disorders involving  
XX CC eosinophils, such as allergic inflammatory and hypersensitivity  
XX CC reactions, certain types of leukemia, and certain infectious disorders  
XX CC involving CCR3, e.g. HIV or respiratory syncytial virus infection.  
XX CC Expression and modulation of CCR3 is a useful tool in assessing  
XX CC eosinophil targeting and in regulating eosinophil-mediated reactions and  
XX CC diseases

XX SQ Sequence 51 BP; 13 A; 12 C; 11 G; 0 T; 15 U; 0 Other;

Query Match 100.0%; Score 21; DB 6; Length 51;  
Best Local Similarity 81.0%; Pred. No. 0.024;  
Matches 17; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGAACTTATCGAAATACA 21  
DB 31 GCAAGAACTTATCGAAATACA 51

## RESULT 5

AAT31335  
ID AAT31335 standard; cDNA; 1193 BP.

XX AC AAT31335;

XX DT 15-NOV-1996 (first entry)

XX DE CC-chemokine receptor 3 cDNA clone.

XX KW CC-chemokine receptor 3; CKP-3; Eos-L2; inhibitor; antisense;  
XX KW antiinflammatory; eosinophil; ss.

XX OS Homo sapiens.

XX PH Key Location/Qualifiers

XX CDS 92..1159

XX FT /\*tag= a

XX FT 918..919

XX FT variation

XX FT /\*tag= b  
XX FT /note= "CCR-3 cDNA clone has GC at positions 918-919,  
XX FT coding for serine (AGC) at position 276; a genomic clone  
XX FT has CG at these positions, coding for threonine (AGC)"

XX PN WO9622371-A2.

XX PD 25-JUL-1996.

XX PF 19-JAN-1996; 96WO-US000608.

XX PR 19-JAN-1995; 95US-00375199.

XX PA (LEUK-) LEUKOSITE INC.

XX PA (EGHM) BRIGHAM & WOMENS HOSPITAL.

XX PA (CHIL-) CHILDRENS MEDICAL CENT.

XX PI Gerard CJ, Gerard NP, Mackay CR, Ponath PD, Post TW, Qin S;

XX DR WPI; 1996-354528/35.

XX DR P-PSDB; AAW03377.

XX PT Mammalian chemokine receptor-3 and related nucleic acids - useful to  
XX PT identify receptor inhibitors to treat inflammatory disease, e.g.  
XX PT autoimmune disorders, certain cancers, etc.

XX PS Claim 1; Page 111-113; 153pp; English.

XX CC A genomic DNA clone (AAT31335) codes for a novel receptor (AAW03377),  
XX CC designated Eos L2 or C-C chemokine receptor 3 (CCR-3), involved in  
XX CC leukocyte migration associated with inflammation. It was isolated from a  
XX CC human library constructed from eosinophils obtd. from a patient with  
XX CC hyper-eosinophilic syndrome using a probe (p4 cDNA) encoding the MIP-  
XX CC alpha/RANTES receptor. A CCR-3 genomic clone (AAT31334) was also  
XX CC isolated, and a consensus sequence is given in AAT31336. The cDNA and  
XX CC genomic clones can be used for the prodn. of recombinant CCR-3 in host  
XX CC cells, or to design antisense sequences useful for treating inflammatory  
XX CC disease

XX SQ Sequence 1193 BP; 274 A; 310 C; 275 G; 334 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 2; Length 1193;

Best Local Similarity 100.0%; Pred. No. 0.021;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGAACTTATCGAAATACA 21

DB 15 GCAAGAACTTATCGAAATACA 35

## RESULT 6

AAV07403

ID AAV07403 standard; cDNA; 1193 BP.

XX

AC AAV07403;  
 XX  
 XX  
 DT 28-SEP-1998 (first entry)  
 XX  
 XX Human C-C chemokine receptor 3 cDNA.  
 DE  
 XX  
 XX C-C chemokine receptor 3; CCR3; Eos L2; human;  
 KW G protein-coupled receptor; leukocyte; antibody; antagonist;  
 KW inflammation; allergy; asthma; graft rejection; infection;  
 KW autoimmune disease; drug screening; therapy; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 XX  
 XX Key Location/Qualifiers  
 FT 92.1159  
 FT CDS /\*tag= a  
 XX  
 XX WO9814480-A1.  
 XX  
 XX 09-APR-1998.  
 XX  
 XX 24-SEP-1997; 97WO-US017103.  
 XX  
 XX 30-SEP-1996; 96US-00720565.  
 XX  
 XX (LEUK-) LEUKOSITE INC.  
 XX  
 XX Mackay CR, Ponath PD;  
 XX  
 XX WPI; 1998-286418/25.  
 DR P-PSDB; AAW51745.  
 DR  
 XX Antibodies to chemokine receptor-3 protein - useful for diagnosis and  
 PT treatment of inflammatory conditions, e.g. allergy, asthma, autoimmune  
 PT disease, graft rejection or cancer.  
 PT  
 XX Example 8; Page 134-136; 185pp; English.  
 PS  
 XX  
 XX This cDNA codes for novel human C-C chemokine receptor 3 (see AAW51745),  
 CC also designated CCR-3, CCR3 or Eos L2, that binds and mediates chemotaxis  
 CC in response to chemokines such as eotaxin, RANTES and MCP-3. The cDNA was  
 CC isolated from a human eosinophil cDNA library constructed from  
 CC eosinophils obtained from a patient with hypereosinophilic syndrome, and  
 CC using CCR-1 cDNA as probe. A genomic DNA sequence (see AAV07402) is also  
 CC provided as well as a consensus sequence (see AAV07404) for CCR-3. The  
 CC invention relates to isolated and/or recombinant nucleic acids encoding  
 CC CCR-3, isolated or recombinant CCR-3 polypeptides, recombinant nucleic  
 CC acid constructs, host cells useful for production of recombinant CCR-3  
 CC proteins, to antibodies reactive with the receptors, and to methods of  
 CC using these products to identify ligands, antagonists and agonists of  
 CC receptor function. Inhibitors of CCR-3 can be used to treat: inflammatory  
 CC or allergic diseases and conditions, including respiratory allergic  
 CC diseases such as asthma, allergic rhinitis, hypersensitivity lung  
 CC disease, hypersensitivity pneumonitis, eosinophilic pneumonia (e.g.  
 CC Loeffler's syndrome, chronic eosinophilic pneumonia, interstitial lung  
 CC disease (ILD) e.g. idiopathic pulmonary fibrosis or ILD associated with  
 CC rheumatoid arthritis, systemic lupus erythematosus, ankylosing  
 CC spondylitis, systemic sclerosis, Sjogren's syndrome, polymyositis or  
 CC dermatomyositis), systemic anaphylaxis or hypersensitivity responses,  
 CC drug allergy, insect sting allergy, inflammatory bowel disease, such as  
 CC Crohn's disease and ulcerative colitis, spondyloarthropathy, scleroderma,  
 CC psoriasis, inflammatory dermatosis such as dermatitis, eczema, atopic  
 CC dermatitis, allergic contact dermatitis, urticaria, vasculitis (e.g.  
 CC necrotizing cutaneous and hypersensitivity vasculitis); eosinophilic  
 CC myositis and eosinophilic fasciitis; autoimmune diseases such as  
 CC rheumatoid arthritis, psoriatic arthritis, multiple sclerosis, systemic  
 CC lupus erythematosus, myasthenia gravis, juvenile onset diabetes,  
 CC glomerulonephritis, autoimmune thyroiditis and Behcet's disease; graft  
 CC rejection, including allograft rejection or graft-versus-host disease;  
 CC cancers with leukocyte infiltration of the skin or organs; and also  
 CC reperfusion injury, atherosclerosis, certain haematologic malignancies,  
 CC septic shock and endotoxic shock. Promoters of CCR-3 function can be used  
 CC for treating: immunosuppression e.g. in AIDS patients or individuals

CC undergoing radiation therapy, chemotherapy, therapy for autoimmune  
 CC disease or other drug therapy, and immunosuppression due congenital  
 CC deficiency in receptor function or other causes; and infectious diseases  
 CC such as parasitic diseases, including helminth infections, such as  
 CC nematodes (round worms). The agents can also be used for detection and  
 CC diagnosis  
 XX  
 XX Sequence 1193 BP; 274 A; 310 C; 275 G; 334 T; 0 U; 0 Other;  
 SQ  
 Query Match 100.0%; Score 21; DB 2; Length 1193;  
 Best Local Similarity 100.0%; Pred. No. 0.021;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GCAAGAACTTATCGAAATACA 21  
 Db 15 GCAAGAACTTATCGAAATACA 35  
 RESULT 7  
 ABQ78513  
 ID ABQ78513 standard; DNA; 2895 BP.  
 XX  
 XX AC ABQ78513;  
 XX  
 XX DT 25-NOV-2002 (first entry)  
 XX  
 XX DE Nucleotide sequence of the human CCR3 gene promoter.  
 XX  
 XX KW Human; CC chemokine receptor 3; CCR3; allergic disorder;  
 KW inflammatory disorder; eosinophil; hypersensitivity; leukemia;  
 KW infectious disorder; HIV; respiratory syncytial virus infection;  
 KW promoter; ss.  
 XX  
 XX OS Homo sapiens.  
 XX  
 XX FH Key Location/Qualifiers  
 FT misc\_signal 1640..1645  
 FT /\*tag= a  
 FT /note= "splice donor consensus site"  
 XX  
 XX PN WO200262848-A2.  
 XX  
 XX PD 15-AUG-2002.  
 XX  
 XX PF 06-FEB-2002; 2002WO-US0003442.  
 XX  
 XX PR 07-FEB-2001; 2001US-0267073P.  
 XX  
 XX PR 05-FEB-2002; 2002US-00068067.  
 XX  
 XX PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
 XX  
 XX PI Rothenberg MB, Zimmerman N;  
 XX  
 XX WPI; 2002-657524/70.  
 XX  
 XX New CC chemokine receptor 3 (CCR3) regulatory site in an untranslated  
 PT exon 1, exon 2, exon 3 or promoter of a human CCR3 gene, capable  
 PT of binding to regulatory elements, useful for preventing e.g. allergic  
 PT inflammatory reactions.  
 XX  
 XX PS Disclosure; Fig 4; 56pp; English.  
 XX  
 XX The present sequence represents the promoter of the human CC chemokine  
 CC receptor 3 (CCR3) gene. CCR3 is expressed on cells involved in allergic  
 CC and/or inflammatory disorders. The gene comprises 4 exons, with the  
 CC coding region present on exon 4. The specification describes methods of  
 CC regulating the expression of CCR3. The regulatory site is derived from an  
 CC untranslated exon 1, exon 2, exon 3 or promoter of a human CCR3 gene.  
 CC Regulating the expression of the chemokine receptor CCR3 is useful for  
 CC preventing or treating disorders involving eosinophils, such as allergic  
 CC inflammatory and hypersensitivity reactions, certain types of leukemia,  
 CC and certain infectious disorders involving CCR3, e.g. HIV or respiratory  
 CC syncytial virus infection. Expression and modulation of CCR3 is a useful

CC tool in assessing eosinophil targeting and in regulating eosinophil-mediated reactions and diseases

XX Sequence 2895 BP; 829 A; 590 C; 556 G; 920 T; 0 U; 0 Other;

SQ Query Match 100.0%; Score 21; DB 6; Length 2895;  
Best Local Similarity 100.0%; Pred. No. 0.02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGAACTTATCGAATAACA 21  
|||||

Db 1591 GCAGAACTTATCGAATAACA 1611  
|||||

RESULT 8

ABL12512/c  
ID ABL12512 standard; cDNA; 3140 BP.

XX AC ABL12512;

XX DT 26-MAR-2002 (first entry)

XX DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 32018.

XX KW Drosophila; developmental biology; cell signalling; insecticide;

XX KW pharmaceutical; gene; ss.

XX OS Drosophila melanogaster.

XX PN WO200171042-A2.

XX PD 27-SEP-2001.

XX PF 23-MAR-2001; 2001WO-US009231.

XX PR 23-MAR-2000; 2000US-0191637P.

XX PR 11-JUL-2000; 2000US-00614150.

XX PA (PEKE ) PE CORP NY.

XX PI Venter JC, Adams M, Li PWD, Myers EW;

XX DR WPI; 2001-656860/75.

XX DR P-PSDB; ABB68409.

XX PT New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.

XX PS Claim 1; SEQ ID NO 32018; 21pp + Sequence Listing; English.

XX CC The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 3140 BP; 789 A; 738 C; 769 G; 844 T; 0 U; 0 Other;

XX Query Match 81.0%; Score 17; DB 4; Length 3140;  
Best Local Similarity 100.0%; Pred. No. 3.3;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AAGAACTTATCGAATA 19  
|||||

Db 2243 AAGAACTTATCGAATA 2227  
|||||

RESULT 9

ABL12414/c  
ID ABL12414 standard; cDNA; 4400 BP.

XX AC ABL12414;

XX DT 26-MAR-2002 (first entry)

XX DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 31724.

XX KW Drosophila; developmental biology; cell signalling; insecticide;

XX KW pharmaceutical; gene; ss.

XX OS Drosophila melanogaster.

XX PN WO200171042-A2.

XX PD 27-SEP-2001.

XX PF 23-MAR-2001; 2001WO-US009231.

XX PR 23-MAR-2000; 2000US-0191637P.

XX PR 11-JUL-2000; 2000US-00614150.

XX PA (PEKE ) PE CORP NY.

XX PI Venter JC, Adams M, Li PWD, Myers EW;

XX DR WPI; 2001-656860/75.

XX DR P-PSDB; ABB68311.

XX PT New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions.

XX PS Claim 1; SEQ ID NO 31724; 21pp + Sequence Listing; English.

XX CC The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 4400 BP; 1037 A; 1066 C; 1109 G; 1188 T; 0 U; 0 Other;

XX Query Match 81.0%; Score 17; DB 4; Length 4400;  
Best Local Similarity 100.0%; Pred. No. 3.3;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AAGAACTTATCGAATA 19  
|||||

Db 765 AAGAACTTATCGAATA 749  
|||||

RESULT 10

AAA81538/c  
ID AAA81538 standard; DNA; 5532 BP.

XX AC AAA81538;

XX DT 04-DEC-2000 (first entry)

XX DE N. meningitidis partial DNA sequence grm\_95 SEQ ID NO:85.

XX KW Neisseria meningitidis; Neisseria gonorrhoeae; genome; immunogenic;  
antigen; vaccine; diagnosis; infection; antibacterial; identification;

XX KW Meningococcus B; MenB; ds.



CC outer membrane proteins currently used

XX Sequence 349980 BP; 87189 A; 93501 C; 84627 G; 84663 T; 0 U; 0 Other;

SQ Query Match 76.2%; Score 16; DB 3; Length 349980;

XX Best Local Similarity 100.0%; Pred. No. 9.5;

XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGAACTTATCGAA 16

Db 81221 GCAAGAACTTATCGAA 81206

RESULT 13

AAC94557

ID AAC94557 standard; cDNA; 537 BP.

XX AC AAC94557;

XX DT 19-FEB-2001 (first entry)

XX DE Cat flea hindgut and Malpighian tubule (HMT) cDNA, SEQ ID NO:1052.

XX KW Cat flea; hindgut and Malpighian tubule nucleic acid; HMT;

XX KW flea infestation; vaccine; antiparasitic; therapeutic target; diagnosis;

XX KW detection; ss.

XX OS Ctenocephalides felis.

XX PN WO2000061621-A2.

XX PD 19-OCT-2000.

XX PF 07-APR-2000; 2000WO-US009437.

XX PR 09-APR-1999; 99US-0128704P.

XX PA (HESK-) HESKA CORP.

XX PI Brandt KS, Gaines PJ, Stinchcomb DT, Wisniewski N;

XX WPI; 2000-656323/63.

XX Flea Malpighian tubule and head and nerve cord tissue derived nucleic

XX acids useful for the prevention, diagnosis and treatment of flea

XX infestations.

XX Claim 26; Page 587; 964pp; English.

XX The invention relates to novel cat flea (Ctenocephalides felis) nucleic

XX acids which are expressed in hindgut and Malpighian tubule (HMT) tissue

XX or head and nerve cord (HNC) tissue. The invention also relates to the

XX encoded proteins. The invention additionally encompasses expression

XX constructs, recombinant viruses and recombinant cells comprising the

XX nucleic acids of the invention, recombinant production of the proteins,

XX antibodies against the proteins, a method of identifying inhibitors of

XX the proteins, and compositions comprising the inhibitors for

XX administration to an animal. The nucleic acids, and the proteins they

XX encode may be used in the prevention, treatment and diagnosis of diseases

XX associated with flea infestations. For example, the nucleic acids may be

XX used to produce an HMT or HNC protein according to standard recombinant

XX DNA methodology by inserting the nucleic acids into a host cell and

XX culturing the cell to express the protein. The HMT and HNC nucleic acids

XX may also be used as DNA probes in diagnostic assays (e.g., PCR) to detect

XX and quantitate the presence of cat flea or other homologous nucleic acid

XX sequences in samples. They may also be used to study the expression and

XX function of the proteins and their role in metabolism. The HMT and HNC

XX proteins may be used as antigens in the production of specific

XX antibodies, and in assays to identify modulators (agonists and

XX antagonists) of HMT and/or HNC protein expression and activity. The anti-

XX HMT/HNC protein antibodies and antagonists may also be used to

XX downregulate protein expression and activity. The antibodies may also be

XX used as diagnostic agents for detecting the presence of flea polypeptides

CC in samples (e.g., by enzyme linked immunosorbent assay (ELISA)). The

XX present sequence represents a cat flea HMT cDNA of the invention

SQ Sequence 537 BP; 164 A; 86 C; 101 G; 185 T; 0 U; 1 Other;

XX Query Match 71.4%; Score 15; DB 3; Length 537;

XX Best Local Similarity 100.0%; Pred. No. 48;

XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AACTTATCGAATAC 20

Db 144 AACTTATCGAATAC 158

RESULT 14

ACF70596

ID ACF70596 standard; DNA; 864 BP.

XX AC ACF70596;

XX DT 20-NOV-2003 (first entry)

XX DE Photorhabdus luminescens nucleotide sequence #9063.

XX KW Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;

XX KW detection; food; gene expression; plant; animal; microorganism; toxin;

XX KW antibiotic; biopesticide; virulence factor; disease model; plague;

XX KW whooping cough; gene; ds.

XX OS Photorhabdus luminescens.

XX PN WO200294867-A2;

XX PD 28-NOV-2002.

XX PF 07-FEB-2002; 2002WO-IB003040.

XX PR 07-FEB-2001; 2001FR-00001659.

XX PA (INSP ) INST PASTEUR.

XX PA (CNRS ) CNRS CENT NAT RECH SCI.

XX PI Duchaud B, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A;

XX PI Buchrieser C;

XX WPI; 2003-148459/14.

XX Genomic sequence of Photorhabdus luminescens and encoded polypeptides,

XX useful e.g. as therapeutic antimicrobials and agricultural pesticides.

XX Claim 2; SEQ ID NO 9063; 1205pp; French.

XX The invention relates to the isolation of genes and their encoded

XX proteins from Photorhabdus luminescens. The isolated sequences are

XX sources of probes and primers for detecting the genome of P. luminescens

XX and related species; to study polymorphisms; for gene analysis and for

XX detection/amplification of the genes. Antibodies (Ab) raised against the

XX polypeptides encoded by the genes are used for detection/identification

XX of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that

XX carry a gene-containing vector are used to select compounds that

XX modulate, regulate, induce or inhibit expression of the genes in plants,

XX animals or microorganisms other than P. luminescens and are able to alter

XX response or sensitivity to toxins and antibiotics produced by P.

XX luminescens. Cells transformed to express the genes are useful for

XX recombinant production of the proteins, particularly toxins and

XX antibacterials useful as insecticides, bactericides and fungicides. The

XX genes, proteins, vectors containing the genes and Ab are also useful

XX therapeutically (to treat microbial infection by bacteria or fungi that

XX are sensitive to P. luminescens-encoded toxins or antibiotics) and as

XX biopesticides. Other uses of the genes and the proteins are as virulence

XX factors and for identifying targets of human diseases for which P.

XX luminescens is a model (particularly plague and whooping cough). This

XX sequence represents one of the isolated P. luminescens genes

```
XX
SQ Sequence 864 BP; 251 A; 153 C; 188 G; 272 T; 0 U; 0 Other;
Query Match 71.4%; Score 15; DB 7; Length 864;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGAAGTTATCGAAA 17
Db 446 AAGAAGTTATCGAAA 460

RESULT 15
ABL25529
ID ABL25529 standard; DNA; 1056 BP.
XX
AC ABL25529;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 28050.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ds.
XX
OS Drosophila melanogaster.
XX
WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
XX
PT 11-JUL-2000; 2000US-00614150.
XX
PA (PEKE ) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT Genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
PS Claim 1; SEQ ID NO 28060; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC RBB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1056 BP; 227 A; 256 C; 249 G; 324 T; 0 U; 0 Other;
Query Match 71.4%; Score 15; DB 4; Length 1056;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CAAGAAGTTATCGAA 16
Db 330 CAAGAAGTTATCGAA 344
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Search completed: August 2, 2004, 18:24:30  
Job time : 104.379 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 2, 2004, 18:10:40 ; Search time 21.181 Seconds  
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550.208 Million cell updates/sec

Title: US-10-068-067-19

Perfect score: 21

Sequence: 1 gcaagaacttcgaaataca 21

Scoring table: OLIGO NUC

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Searched: 682709 seqs, 277475446 residues

Word size : 0

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA.\*

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- 2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq.\*
- 3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq.\*
- 4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq.\*
- 5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq.\*
- 6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	21	100.0	1193	4	US-08-720-565-3
2	15	71.4	8920	2	US-08-446-855A-1
3	15	71.4	8920	3	US-09-150-741-1
4	14	66.7	435	4	US-09-489-039A-6593
5	14	66.7	2793	4	US-08-753-750B-1
6	14	66.7	4820	4	US-08-961-527-19
7	14	66.7	45175	4	US-09-453-702B-116
8	14	65.7	129908	4	US-09-585-858-1
9	13	61.9	207	4	US-09-107-532A-1213
10	13	61.9	400	4	US-08-956-171E-1342
11	13	61.9	1056	3	US-09-293-395-10
12	13	61.9	1056	3	US-09-668-648-10
13	13	61.9	1474	4	US-08-858-207A-144
14	13	61.9	1479	4	US-09-107-532A-3408
15	13	61.9	2153	4	US-09-221-017B-984
16	13	61.9	2538	4	US-09-543-681A-193
17	13	61.9	2951	1	US-08-413-118-105
18	13	61.9	2951	3	US-08-473-446-105
19	13	61.9	5739	4	US-09-634-238-1
20	13	61.9	8703	4	US-08-961-527-177
21	13	61.9	640681	4	US-09-790-988-1
22	12	57.1	31	2	US-08-467-265-9
23	12	57.1	31	3	US-08-467-265-9
24	12	57.1	31	3	US-09-407-891-9
25	12	57.1	38	2	US-08-467-265-6
26	12	57.1	38	3	US-08-467-265-6
27	12	57.1	38	3	US-09-407-891-6

28 12 57.1 145 4 US-08-956-171E-3207 Sequence 3207, Ap  
C 29 12 57.1 160 1 US-08-327-525A-19 Sequence 19, Appl  
C 30 12 57.1 160 1 US-08-327-525A-25 Sequence 25, Appl  
C 31 12 57.1 160 1 US-08-327-525A-26 Sequence 26, Appl  
C 32 12 57.1 160 1 US-08-327-525A-27 Sequence 27, Appl  
C 33 12 57.1 160 2 US-08-531-137B-19 Sequence 19, Appl  
C 34 12 57.1 160 2 US-08-531-137B-25 Sequence 25, Appl  
C 35 12 57.1 160 2 US-08-531-137B-26 Sequence 26, Appl  
C 36 12 57.1 160 2 US-08-531-137B-27 Sequence 27, Appl  
C 37 12 57.1 160 3 US-09-158-765-19 Sequence 19, Appl  
C 38 12 57.1 160 3 US-09-158-765-25 Sequence 25, Appl  
C 39 12 57.1 160 3 US-09-158-765-26 Sequence 26, Appl  
C 40 12 57.1 160 3 US-09-158-765-27 Sequence 27, Appl  
C 41 12 57.1 160 4 US-09-796-071-19 Sequence 19, Appl  
C 42 12 57.1 160 4 US-09-796-071-25 Sequence 25, Appl  
C 43 12 57.1 160 4 US-09-796-071-26 Sequence 26, Appl  
C 44 12 57.1 160 4 US-09-796-071-27 Sequence 27, Appl  
C 45 12 57.1 246 4 US-09-489-039A-4912 Sequence 4912, Ap

#### ALIGNMENTS

RESULT 1  
US-08-720-565-3  
; Sequence 3, Application US/08720565  
; Patent No. 6537764  
; GENERAL INFORMATION:  
; APPLICANT: Gerard, Craig J.  
; APPLICANT: Gerard, No. 6537764ma P.  
; APPLICANT: Mackay, Charles R.  
; APPLICANT: Ponath, Paul D.  
; APPLICANT: Post, Theodore W.  
; APPLICANT: Qin, Shixin  
; TITLE OF INVENTION: G PROTEIN-COUPLED RECEPTOR GENE CCR3 AND  
; TITLE OF INVENTION: ANTAGONISTS THEREOF  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02173  
; COMPUTER READABLE FORM: disk  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/720,565  
; FILING DATE: 30-SEP-1996  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/00608  
; FILING DATE: 19-JAN-1996  
; PRIOR APPLICATION NUMBER: US 08/375,199  
; APPLICATION NUMBER: US 08/375,199  
; FILING DATE: 19-JAN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brook, David E.  
; REGISTRATION NUMBER: 22,592  
; REFERENCE/DOCKET NUMBER: LKS94-05A2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-861-6240  
; TELEFAX: 617-861-9540  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1193 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: 92..1156
; US-08-720-565-3

Query Match      100.0%; Score 21; DB 4; Length 1193;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGAACTTATCGAATACA 21
    |||||
Db 15 GCAAGAACTTATCGAATACA 35
    |||||

RESULT 2
US-08-446-855A-1
; Sequence 1, Application US/08446855A
; Patent No. 5849573
; GENERAL INFORMATION:
; APPLICANT: Stewart, Thomas S
; APPLICANT: Flores, Maria V
; APPLICANT: O'Sullivan, William J
; TITLE OF INVENTION: Nucleotide sequence encoding carbamoyl
; TITLE OF INVENTION: Phosphate synthetase II
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon & Vanderhye PC
; STREET: 1100 No. 5849573th Glebe Road, 8th Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,855A
; FILING DATE: 06-Jul-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mitchard, Leonard C
; REGISTRATION NUMBER: 29,009
; REFERENCE/DOCKET NUMBER: 47-80
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8920 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic
; US-08-446-855A-1

Query Match      71.4%; Score 15; DB 2; Length 8920;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AAGAACTTATCGAAA 17
    |||||
Db 3831 AAGAACTTATCGAAA 3845
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RESULT 3
US-09-150-741-1
; Sequence 1, Application US/09150741
; Patent No. 6183996
; GENERAL INFORMATION:
; APPLICANT: Stewart et al.
; TITLE OF INVENTION: Nucleotide Sequence Encoding Carbamoyl Phosphate

; Patent No. 6183996
; TITLE OF INVENTION: Synthetase II
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/150,741
; CURRENT FILING DATE: 1998-09-10
; EARLIER APPLICATION NUMBER: PL6380
; EARLIER FILING DATE: 1992-12-16
; EARLIER APPLICATION NUMBER: AU93/00617
; EARLIER FILING DATE: 1993-12-02
; EARLIER APPLICATION NUMBER: 08/446,855
; EARLIER FILING DATE: 1995-07-06
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 1
; LENGTH: 8920
; TYPE: DNA
; ORGANISM: Plasmodium falciparum
; US-09-150-741-1

Query Match      71.4%; Score 15; DB 3; Length 8920;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AAGAACTTATCGAAA 17
    |||||
Db 3831 AAGAACTTATCGAAA 3845
    |||||

RESULT 4
US-09-489-039A-6593
; Sequence 6593, Application US/09489039A
; Patent No. 8610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709,2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 6593
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
; US-09-489-039A-6593

Query Match      66.7%; Score 14; DB 4; Length 435;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GAACCTTATCGAAT 18
    |||||
Db 85 GAACCTTATCGAAT 98
    |||||

RESULT 5
US-08-753-750B-1
; Sequence 1, Application US/08753750B
; Patent No. 8610506
; GENERAL INFORMATION:
; APPLICANT: Lo, Reggie Y.C.
; APPLICANT: Schryvers, Anthony B.
; APPLICANT: Potter, Andrew A.
; TITLE OF INVENTION: TRANSFERRIN BINDING PROTEINS OF
; TITLE OF INVENTION: PASTEURELLA HAEMOLYTICA AND VACCINES CONTAINING THE SAME
; FILE REFERENCE: A34762 321645.0105
; CURRENT APPLICATION NUMBER: US/08/753,750B
; CURRENT FILING DATE: 1996-11-29
; PRIOR APPLICATION NUMBER: CA 2,164,274
; PRIOR FILING DATE: 1995-12-01
; PRIOR APPLICATION NUMBER: 60/008,569
```

; PRIOR FILING DATE: 1995-12-01  
 ; NUMBER OF SEQ ID NOS: 58  
 ; SOFTWARE: FASTSEQ for Windows Version 4.0  
 ; SEQ ID NO 1  
 ; LENGTH: 2793  
 ; TYPE: DNA  
 ; ORGANISM: Pasteurella haemolytica  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: 2544  
 ; OTHER INFORMATION: a, c, g or t  
 US-08-753-750B-1

Query Match 66.7%; Score 14; DB 4; Length 2793;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GAACCTATCGAAAT 18  
 |||||  
 DB 1895 GAACCTATCGAAAT 1908

RESULT 6  
 US-08-961-527-19  
 ; Sequence 19, Application US/08961527  
 ; Patent No. 6420135  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Charles Kunsch  
 ; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences  
 ; NUMBER OF SEQUENCES: 391  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Human Genome Sciences, Inc.  
 ; STREET: 9410 Key West Avenue  
 ; CITY: Rockville  
 ; STATE: Maryland  
 ; COUNTRY: USA  
 ; ZIP: 20850

; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
 ; COMPUTER: HP Vectra 486/33  
 ; OPERATING SYSTEM: MSDOS version 6.2  
 ; SOFTWARE: ASCII Text  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/961.527  
 ; FILING DATE:  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION NUMBER:  
 ; FILLING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Brookes, A. Anders  
 ; REGISTRATION NUMBER: 36,373  
 ; REFERENCE/DOCKET NUMBER: PB340P1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (301) 309-8504  
 ; TELEFAX: (301) 309-8512  
 ; INFORMATION FOR SEQ ID NO: 19:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 4820 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear

US-08-961-527-19  
 Query Match 66.7%; Score 14; DB 4; Length 4820;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACTTATCGAAATAC 20  
 |||||  
 DB 3955 ACTTATCGAAATAC 3968

RESULT 7  
 US-09-453-702B-116/c  
 ; Sequence 116, Application US/09453702B  
 ; Patent No. 6365723  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Blattner, Frederick R.  
 ; Burland, Valerie  
 ; Perna, Nicole T.  
 ; Plunkett, Guy  
 ; Welch, Rod  
 ; TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157  
 ; NUMBER OF SEQUENCES: 265  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Quarles & Brady  
 ; STREET: 1 South Pinckney Street  
 ; CITY: Madison  
 ; STATE: WI  
 ; COUNTRY: US  
 ; ZIP: 53701-2113  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Word Perfect 8.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/453,702B  
 ; FILING DATE: 03-Dec-1999  
 ; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 60/110,955  
 ; FILING DATE: 04-DEC-1998  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Seay, Nicholas J.  
 ; REGISTRATION NUMBER: 27386  
 ; REFERENCE/DOCKET NUMBER: 960296.95017  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (608) 251-5000  
 ; TELEFAX: (608) 251-9166  
 ; INFORMATION FOR SEQ ID NO: 116:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 45175  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 116:  
 US-09-453-702B-116

Query Match 66.7%; Score 14; DB 4; Length 45175;  
 Best Local Similarity 100.0%; Pred. No. 18;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGAACTTATCG 14  
 |||||  
 DB 34538 GCAAGAACTTATCG 34525

RESULT 8  
 US-09-585-858-1  
 ; Sequence 1, Application US/09585858  
 ; Patent No. 6492161  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sigrundur Hjordisdotter  
 ; APPLICANT: Gudmundur O. Hreggvidsson  
 ; APPLICANT: Olafur H. Fridjonsson  
 ; APPLICANT: Arthor Aevarsson  
 ; APPLICANT: Jakob K. Kristjansson  
 ; TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic  
 ; FILE REFERENCE: 2739.1001-001  
 ; CURRENT APPLICATION NUMBER: US/09/585,858  
 ; CURRENT FILING DATE: 2000-12-18  
 ; PRIOR APPLICATION NUMBER: 60/137,120

;; PRIOR FILING DATE: 1999-06-02  
;; NUMBER OF SEQ ID NOS: 73  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 1  
;; LENGTH: 129908  
;; TYPE: DNA  
;; ORGANISM: Bacteriophage RM378  
US-09-585-858-1

Query Match 66.7%; Score 14; DB 4; Length 129908;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GAACCTTATCGAAAT 18  
| | | | | | | | | | | | | | | | | | | | | |  
DB 11282 GAACCTTATCGAAAT 11295

## RESULT 9

US-09-107-532A-1213  
; Sequence 1213, Application US/09107532A  
; Patent No. 6593275  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

;; NUMBER OF SEQUENCES: 7310  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: GENOME THERAPEUTICS CORPORATION

;; STREET: 100 Beaver Street  
;; CITY: Waltham  
;; STATE: Massachusetts  
;; COUNTRY: USA  
;; ZIP: 02354

;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: CD-ROM ISO9660  
;; COMPUTER: PC  
;; OPERATING SYSTEM: <Unknown>  
;; SOFTWARE: ASCII  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/107,532A  
;; FILING DATE: 30-Jun-1998

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 60/085,598  
;; FILING DATE: 14 May 1998  
;; APPLICATION NUMBER: 60/051571  
;; FILING DATE: July 2, 1997

;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Ariniello, Pamela Deneke  
;; REGISTRATION NUMBER: 40,489  
;; REFERENCE/DOCKET NUMBER: GTC-012  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (781)893-5007  
;; TELEFAX: (781)893-8277

;; INFORMATION FOR SEQ ID NO: 1213:  
;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 207 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: double  
;; TOPOLOGY: circular  
;; MOLECULE TYPE: DNA (genomic)

;; HYPOTHETICAL: NO  
;; ANTI-SENSE: NO  
;; ORIGINAL SOURCE:

;; ORGANISM: Enterococcus faecium  
;; FEATURE:

;; NAME/KEY: misc feature  
;; LOCATION: (B) LOCATION 1...207  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 1213:  
US-09-107-532A-1213

Query Match 61.9%; Score 13; DB 4; Length 207;  
Best Local Similarity 100.0%; Pred. No. 74;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCAAGAACTTATC 13  
| | | | | | | | | | | | | | | | | | | | | |  
DB 139 GCAAGAACTTATC 151

## RESULT 10

US-08-956-171E-1342  
; Sequence 1342, Application US/08956171E  
; Patent No. 6593114  
; GENERAL INFORMATION:  
; APPLICANT: Charles Kunsch

;; Gil H. Choi  
;; Patrick S. Dillon  
;; Craig A. Rosen  
;; Steven C. Barash  
;; Michael R. Fannon  
;; ADDRESSEE: Human Genome Sciences, Inc.  
;; STREET: 9410 Key West Avenue  
;; CITY: Rockville  
;; STATE: Maryland  
;; COUNTRY: USA  
;; ZIP: 20850

;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
;; COMPUTER: HP Vectra 486/33  
;; OPERATING SYSTEM: MSDOS version 6.2  
;; SOFTWARE: ASCII Text  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/956,171E  
;; FILING DATE: 20-Oct-1997

;; CLASSIFICATION: <Unknown>  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 60/009,861  
;; FILING DATE: January 5, 1996

;; APPLICATION NUMBER: 08/781,986  
;; FILING DATE: January 3, 1997  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Mark J. Hyman  
;; REGISTRATION NUMBER: 46,789

;; REFERENCE/DOCKET NUMBER: PB248P1  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (240) 314-1224  
;; TELEFAX: (301) 309-8439

;; INFORMATION FOR SEQ ID NO: 1342:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 400 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: double  
;; TOPOLOGY: linear

;; SEQUENCE DESCRIPTION: SEQ ID NO: 1342:  
US-08-956-171E-1342

Query Match 61.9%; Score 13; DB 4; Length 400;  
Best Local Similarity 100.0%; Pred. No. 73;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GAACCTTATCGAAA 17  
| | | | | | | | | | | | | | | | | | | | | |  
DB 87 GAACCTTATCGAAA 99

## RESULT 11

US-09-293-395-10  
; Sequence 10, Application US/09293395  
; Patent No. 6174860  
; GENERAL INFORMATION:  
; APPLICANT: Kramer, Vance  
; APPLICANT: Morgan, Michael

APPLICANT: Anderson, Arne  
TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS  
FILE REFERENCE: PB/5-30472A/USN  
CURRENT APPLICATION NUMBER: US/09/293,395  
CURRENT FILING DATE: 1999-04-16  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 10  
LENGTH: 1056  
TYPE: DNA  
ORGANISM: Xenorhabdus poinarii  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(1053)  
OTHER INFORMATION: JHE-like orf2 of pCIB9354  
US-09-293-395-10

Query Match 61.9%; Score 13; DB 3; Length 1056;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGAACTTATCGA 15  
|||||  
Db 536 AAGAACTTATCGA 548

RESULT 12  
US-09-668-648-10  
Sequence 10, Application US/09668648  
Patent No. 6277823  
GENERAL INFORMATION:  
APPLICANT: Kramex, Vance  
APPLICANT: Morgan, Michael  
APPLICANT: Anderson, Arne  
TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS  
FILE REFERENCE: PB/5-30472A/USN  
CURRENT APPLICATION NUMBER: US/09/668,648  
CURRENT FILING DATE: 2000-09-22  
PRIOR FILING DATE: 1999-04-16  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 10  
LENGTH: 1056  
TYPE: DNA  
ORGANISM: Xenorhabdus poinarii  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(1053)  
OTHER INFORMATION: JHE-like orf2 of pCIB9354  
US-09-668-648-10

Query Match 61.9%; Score 13; DB 3; Length 1056;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGAACTTATCGA 15  
|||||  
Db 536 AAGAACTTATCGA 548

RESULT 13  
US-08-858-207A-144/c  
Sequence 144, Application US/08858207A  
Patent No. 6348328  
GENERAL INFORMATION:  
APPLICANT: Black, Michael  
APPLICANT: Hodgson, John  
APPLICANT: Knowles, David  
APPLICANT: Nicholas, Richard  
APPLICANT: Stodola, Robert

TITLE OF INVENTION: No. 6348328el Compounds  
NUMBER OF SEQUENCES: 552  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406-0939  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/859,207A  
FILING DATE: 09-MAY-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/017670  
FILING DATE: 14-MAY-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Gimmi, Edward R.  
REGISTRATION NUMBER: 38,891  
REFERENCE/DOCKET NUMBER: PS0475  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-4478  
TELEFAX: 610-270-5090  
TELEX:  
INFORMATION FOR SEQ ID NO: 144:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1474 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-858-207A-144

Query Match 61.9%; Score 13; DB 4; Length 1474;  
Best Local Similarity 100.0%; Pred. No. 71;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGAACTTATCGA 15  
|||||  
Db 1135 AAGAACTTATCGA 1123

RESULT 14  
US-09-107-532A-3408  
Sequence 3408, Application US/09107532A  
Patent No. 6583275  
GENERAL INFORMATION:  
APPLICANT: Lynn A Doucette-Stamm and David Bush  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 7310  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
STREET: 100 Beaver Street  
CITY: Waltham  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02354  
COMPUTER READABLE FORM:  
MEDIUM TYPE: CD-ROM ISO9660  
COMPUTER: PC  
OPERATING SYSTEM: <Unknown>  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/107,532A  
FILING DATE: 30-Jun-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/085,598  
FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571  
FILING DATE: July 2, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ariniello, Pamela Deneke  
REGISTRATION NUMBER: 40,489  
REFERENCE/DOCKET NUMBER: GTC-012  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (781)893-5007  
TELEFAX: (781)893-8277  
INFORMATION FOR SEQ ID NO: 3408:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1479 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Enterococcus faecium  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (B) LOCATION 1...1479  
SEQUENCE DESCRIPTION: SEQ ID NO: 3408:

US-09-107-532A-3408

Query Match 61.9%; Score 13; DB 4; Length 1479;  
Best Local Similarity 100.0%; Pred. No. 71;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACTTATCGAAATA 19

Db 1112 ACTTATCGAAATA 1124

## RESULT 15

US-09-221-017B-984  
Sequence 984, Application US/09221017B  
Patent No. 6444799  
GENERAL INFORMATION:  
APPLICANT: Ross, Bruce C.  
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF  
NUMBER OF SEQUENCES: 1120  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 PAGE MILL ROAD  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1019  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/221,017B  
FILING DATE: 23-DEC-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PP1182  
FILING DATE: 31-DEC-1997  
PRIOR APPLICATION DATA: PP1546  
FILING DATE: 30-JAN-1998  
PRIOR APPLICATION DATA: PP2911  
FILING DATE: 09-APR-1998  
PRIOR APPLICATION DATA: PCT/AU98/01023  
FILING DATE: 10-DEC-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Monroy, Gladys H

REGISTRATION NUMBER: 32,430  
REFERENCE/DOCKET NUMBER: 27340-20021.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-813-5600  
TELEFAX: 650-494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 984:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2153 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: UNKNOWN  
ORIGINAL SOURCE:  
ORGANISM: PORYPHYROMONAS GINGIVALIS  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1...2153  
US-09-221-017B-984

Query Match 61.9%; Score 13; DB 4; Length 2153;  
Best Local Similarity 100.0%; Pred. No. 71;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AGAAGTTATCGAA 16

Db 1085 AGAAGTTATCGAA 1097

Search completed: August 2, 2004, 20:30:06  
Job time : 22.181 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 2, 2004, 18:06:45 ; Search time 867.879 Seconds

(without alignments)  
722.573 Million cell updates/sec

Title: US-10-068-067-19

Perfect score: 21

Sequence: 1 gcaagaacttatcgaaataca 21

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:  
1: em\_estba:\*  
2: em\_estum:\*  
3: em\_estin:\*  
4: em\_estov:\*  
5: em\_estmu:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hci:\*  
9: gb\_estl:\*  
10: gb\_est2:\*  
11: gb\_hci:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estun:\*  
16: em\_eston:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_lman:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gssl:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	876	12	BI906283
2	17	81.0	647	12	BM160641
3	16	76.2	288	9	AV340346
4	16	76.2	404	10	BE344124

15	76.2	406	12	BI179888
16	76.2	477	28	BH743658
16	76.2	486	12	BQ045539
16	76.2	487	10	BE471486
16	76.2	493	13	BX563981
16	76.2	517	12	BM407701
16	76.2	649	12	B4435938
16	76.2	654	14	CA998937
16	76.2	677	12	B1435917
16	76.2	685	28	BZ387666
16	76.2	694	10	BG031536
16	76.2	712	9	AU057789
16	76.2	721	9	AL932228
16	76.2	737	12	BG599509
16	76.2	756	12	BG666673
16	76.2	796	14	CB674182
16	76.2	815	14	CK265108
16	76.2	829	10	BE622748
16	76.2	843	28	CC435132
16	76.2	845	14	CK276849
16	76.2	923	14	CK264361
16	76.2	967	14	CK272439
15	71.4	169	9	AV162852
15	71.4	299	29	BX288585
15	71.4	306	29	AL950150
15	71.4	323	29	CC812736
15	71.4	335	9	AU110785
15	71.4	340	28	BH697529
15	71.4	387	28	AQ440255
15	71.4	412	9	AA281990
15	71.4	424	28	BH833079
15	71.4	432	28	BH633995
15	71.4	446	9	AA139325
15	71.4	483	29	AL950151
15	71.4	491	28	AQ866738
15	71.4	498	14	CB336952
15	71.4	501	28	AQ866647
15	71.4	513	28	AZ929038
15	71.4	515	28	BH443715
15	71.4	516	13	BQ988753
15	71.4	517	14	CB358701

ALIGNMENTS

RESULT 1  
BI906283  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

BI906283 876 bp mRNA linear EST 16-OCT-2001  
60363222F1 NIH\_MGC\_118 Homo sapiens cDNA clone IMAGE:5212541 5',  
mRNA sequence.  
BI906283  
BI906283.1 GI:16168946  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999).  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM11533 row: k column: 06  
High quality sequence stop: 800.

FEATURES  
source

Location/Qualifiers  
1. 876  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5212541"  
/tissue\_type="leukocyte"  
/lab\_host="DH10B"  
/clone\_lib="NIH MGC 118"  
/note="Vector: PCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 100.0%; Score 21; DB 12; Length 876;  
Best Local Similarity 100.0%; Pred. No. 0.098;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGAACTTATCGAATACA 21  
DB 16 GCAGAACTTATCGAATACA 36  
|||||

RESULT 2  
LOCUS

BM150641 647 bp mRNA linear EST 04-DEC-2001  
EST563164 PyBS Plasmodium yoelii yoelii cDNA clone PIC789 5' end,  
mRNA sequence.

## DEFINITION

BM150641 GI:17306322

ACCESSION  
VERSION

BM150641.1

KEYWORDS  
SOURCE

Plasmodium yoelii yoelii  
Plasmodium yoelii yoelii

## ORGANISM

Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.

## REFERENCE

1 (bases 1 to 647)  
Carlton, J.M., Daly, T.M., Long, C.A., Bergman, L.W., Vaidya, A.B.,  
Fraser, C.M. and Garucci, D.J.

## AUTHORS

Plasmodium yoelii EST project at TIGR

## TITLE

Unpublished (2001)

## JOURNAL

Contact: Jane Carlton  
Parasite Genomics Group  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-530-9319  
Fax: 301-838-0208  
Email: carlton@tigr.org

## COMMENT

For clone info, please contact the Malaria Research and Reference  
Reagent Resource Center, ATCC  
http://www.malaria.mri.org/mr4pages/index.html  
Seq primer: ADP.

## Location/Qualifiers

1. 647  
/organism="Plasmodium yoelii yoelii"  
/mol\_type="mRNA"  
/strain="17XL"  
/sub\_species="yoelii"  
/db\_xref="taxon:73239"  
/clone="PYCUT89"  
/dev\_stage="Asexual blood stages"  
/lab\_host="E. coli XL-1 Blue"  
/clone\_lib="PyBS"  
/note="Vector: PAD-GAL4; At 20-25% parasitemia, blood was collected from BALB/cBy mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose columns. Total RNA was isolated using the guanidium isothiocyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography."

FEATURES  
source

Location/Qualifiers  
1. 647  
/organism="Plasmodium yoelii yoelii"  
/mol\_type="mRNA"  
/strain="17XL"  
/sub\_species="yoelii"  
/db\_xref="taxon:73239"  
/clone="PYCUT89"  
/dev\_stage="Asexual blood stages"  
/lab\_host="E. coli XL-1 Blue"  
/clone\_lib="PyBS"  
/note="Vector: PAD-GAL4; At 20-25% parasitemia, blood was collected from BALB/cBy mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose columns. Total RNA was isolated using the guanidium isothiocyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography."

First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column. Size-fractionated cDNA was precipitated and ligated to HyriZAP arms directionally using EcoRI-XhoI cleaved arms. After packaging, the phagemid vector (pAD-GAL4) was excised from the HyriZAP vector and plasmid DNA isolated."

## ORIGIN

Query Match 81.0%; Score 17; DB 12; Length 647;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GAACCTTATCGAATACA 21  
DB 139 GAACCTTATCGAATACA 155  
|||||

RESULT 3  
LOCUS

AV340346 288 bp mRNA linear EST 11-NOV-1999  
AV340346 RIKEN full-length enriched, adult male olfactory bulb Mus  
musculus cDNA clone 6430514H24 3', mRNA sequence.

## DEFINITION

AV340346 GI:6380398

ACCESSION  
VERSION

AV340346.1

KEYWORDS  
SOURCE

Mus musculus (house mouse)  
Mus musculus

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 288)

## AUTHORS

Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T.,  
Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F.,  
Ishii, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I.,  
Kai, C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M.,  
Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,  
Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata, K.,  
Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y.,  
Suzuki, H., Suzuki, H., Takahashi, F., Tateo, M., Tomimaga, N.,  
Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yasunishi, A.,  
Yokota, T., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

## TITLE

RIKEN Mouse ESTs (Konno, H., et al. 1999)

## JOURNAL

Unpublished (1999)

## COMMENT

Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic  
Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-resgsc.riken.go.jp  
URL: http://genome.gsc.riken.go.jp/  
Sasaki, N., Izawa, M., Watahiki, M., Ozawa, K., Tanaka, T., Yoneda, Y.,  
Matsura, S., Carninci, P., Muramatsu, M., Okazaki, Y. and  
Hayashizaki, Y.

Transcriptional sequencing: A method for DNA sequencing using RNA  
polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)  
Itoh, M., Katsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,  
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M.,  
Okazaki, Y. and Hayashizaki, Y.  
Automated filtration-based high-throughput plasmid preparation  
system. Genome Res. 9 (5), 463-470 (1999)  
Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,  
19-44 (1999)

Please visit our web site (<http://genome.rtc.riken.go.jp>) for  
further details.

FEATURES  
source

Location/Qualifiers  
1. 288



/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="6430314H24"  
/sex="male"  
/tissue\_type="olfactory brain"  
/dev\_stage="adult"  
/lab\_hosts="DH10B"  
/clone\_lib="RIKEN full-length enriched, adult male olfactory bulb"

/notes="Site 1: Sali; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'-GAGAGAGAGAGACGAGCTCTTTTCTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5'-GAGAGAGAGATCTCGAGTAAATTAATATCCCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: Sali; 3' end: BamHI"

## ORIGIN

Query Match 76.2%; Score 16; DB 9; Length 288;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CAAGAACTTATCGAAA 17  
|||||  
Db 41 CAAGAACTTATCGAAA 56

## RESULT 4

BE344124 404 bp mRNA linear EST 10-MAR-2003  
LOCUS EST409286 potato stolon, Cornell University Solanum tuberosum cDNA  
DEFINITION clone CSTA28M16, mRNA sequence.

ACCESSION BE344124  
VERSION BE344124.1 GI:9253656  
KEYWORDS EST.

SOURCE Solanum tuberosum (potato)  
ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum.

REFERENCE 1 (bases 1 to 404)  
AUTHORS van der Hoeven, R., Bezzerides, J., Bachem, C., Horvath, B., Visser, R., Holt, I.E., Liang, F., Hansen, T.S., Utterback, T., Bowman, C.L., Dean, B., Bougri, O., Buell, C.R., Ronning, C.M., Tanksley, S.D. and Baker, B.

Generation of ESTs from potato swelling stolons  
Unpublished (1999)

CONTACT: Robin Buell

9712 Medical Center Dr, Rockville, MD 20850, USA

Email: potato-array@tigr.org

This clone can be obtained from the University of Arizona Genomics Institute. Orders can be made through URL:

http://genome.arizona.edu/orders/

Location/Qualifiers

## FEATURES

source

1..404  
/organism="Solanum tuberosum"  
/mol\_type="mRNA"  
/cultivar="Bintje"  
/db\_xref="taxon:4113"

/clone="CSTA28M16"  
/tissue\_type="axillary buds of stem explants, swelling stolons"  
/dev\_stage="1 to 3 days"  
/lab\_host="SOLR"  
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; RNA was supplied by Christian Bachem & Beatrice Horvath (Laboratory of Plant Breeding, Dept. of Plant Sciences, Wageningen University, The Netherlands). Total RNA was isolated from developing axillary buds of potato nodal stem cuttings cultured on medium for the introduction of tuber formation as described in Bachem et al. (Plant Journal 1996). Tissue samples were taken of stages corresponding to growing stolons and the early stages of tuber formation."

## ORIGIN

Query Match 76.2%; Score 16; DB 10; Length 404;  
Best Local Similarity 100.0%; Pred. No. 64;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGAACTTATCGAAAT 18  
|||||  
Db 88 AAGAACTTATCGAAAT 103

## RESULT 5

BE1179888 406 bp mRNA linear EST 10-MAR-2003  
LOCUS EST520833 cSTE Solanum tuberosum cDNA clone cSTE20F8 5' sequence,  
DEFINITION mRNA sequence.

ACCESSION BE1179888  
VERSION BE1179888.1 GI:14645699  
KEYWORDS EST.

SOURCE Solanum tuberosum (potato)  
ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum.

REFERENCE 1 (bases 1 to 406)

AUTHORS van der Hoeven, R., Bezzerides, J., Bachem, C., Visser, R., Cho, J., Chiemiango, A., Bougri, O., Buell, C.R., Ronning, C., Tanksley, S. and Baker, B.

Generation of ESTs from in vitro grown microtubers  
Unpublished (2001)

CONTACT: Robin Buell

9712 Medical Center Dr, Rockville, MD 20850, USA

Email: potato-array@tigr.org

This clone can be obtained from the University of Arizona Genomics Institute. Orders can be made through URL:

http://genome.arizona.edu/orders/

Seq primer: M13P-R.

## FEATURES

source

1..406  
/organism="Solanum tuberosum"  
/mol\_type="mRNA"  
/cultivar="Bintje"  
/db\_xref="taxon:4113"  
/clone="cSTE20F8"  
/tissue\_type="axillary buds of stem explants; growing sink-tubers"  
/dev\_stage="7, 8 and 10 days"  
/lab\_host="SOLR"  
/clone\_lib="cSTE"

/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; Tissue supplied by Christian Bachem and Richard Visser (Department of Plant Breeding, Wageningen University, The Netherlands). The cDNA libraries will attempt to capture the induction and initiation/initial growth of the tuber in an in vitro system as described in Bachem et al. (Plant Journal, 1996). Small microtubers

develop from axillary buds attached to stem explants when placed on a high sucrose medium (10%). Visible morphological changes occur synchronously at day five in the axillary buds. The first library, cSTA (1-20) consists of axillary buds harvested on days 1-3. This targets those genes involved in induction of the microtubers. The following libraries, cSTA (21-40) and cSTA (41-60), capture genes involved in tuber initiation and outgrowth. This library is noted as P3 in Tanksley lab notebooks."

## ORIGIN

Query Match 76.2%; Score 16; DB 12; Length 406;  
Best Local Similarity 100.0%; Pred.No. 64;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGAACTTATCGAATA 18

|||||  
Db 90 AAGAACTTATCGAATA 105

## RESULT 6

BH743658/c

LOCUS

DEFINITION BH743658 477 bp DNA linear GSS 25-FEB-2002  
ST25e07.b1 BoBuds01 Brassica oleracea genomic clone gt25e07 5',  
Genomic survey sequence.

ACCESSION BH743658

VERSION BH743658.1 GI:18878272

KEYWORDS GSS.

SOURCE

ORGANISM

Brassica oleracea

Brassica oleracea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 477)

Katarai, M., O'Shaughnessy, A., Palmer, L., Bahret, A., Baker, J.,

Bailly, V., Cummins, D.M., Katzenberger, F., King, L., Kirchoff, K.,

Kuit, K., Miller, B., Muller, S., Nascimento, L., Preston, R.,

Santos, L., Shah, R., Zutavern, T., Dedhia, N., Rabinowicz, P.D. and

McCombie, W.R.

Whole Genome Shotgun Reads from Brassica oleracea (2002b)

Unpublished (2002)

Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

Fax: 516 367 8874

Email: mcombie@cshl.org

Plate: gt25 row: e column: 07

Seq primer: -21univfw

Class: shotgun

High quality sequence stop: 477.

Location/Qualifiers

source

1..477

/organism="Brassica oleracea"

/mol\_type="genomic DNA"

/db\_xref="taxon:3712"

/clone="gt25e07"

/clone\_lib="BoBuds01"

/note="Vector: M13 for x reads, pBluescript for b and g

reads; Site\_1: EcoRV; Whole genome shotgun library from

flowering buds. DNA was purified from a crude nuclear prep

using Brassica oleracea TO1000DH3 buds provided by Thomas

Osborn at the University of Wisconsin. Genomic DNA

provided by Pablo Rabinowicz (CSHL) and shotgun library

prepared in McCombie Lab."

## ORIGIN

QY 4 AAGAACTTATCGAATA 19

|||||

Db 402 AGAACTTATCGAATA 387  
|||||

## RESULT 7

BQ045539

LOCUS

DEFINITION BQ045539 486 bp mRNA linear EST 10-MAR-2003  
EST594656 P. infestans-challenged potato leaf, incompatible  
reaction Solanum tuberosum cDNA clone BPL12K11 5' end, mRNA  
sequence.

ACCESSION BQ045539

VERSION BQ045539.1 GI:19819525

KEYWORDS EST.

SOURCE

ORGANISM

Solanum tuberosum

Solanum tuberosum (potato)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

asterids; lamids; Solanales; Solanaceae; Solanum.

1 (bases 1 to 486)

Zhang, P., Hernandez, M., Tornqvist, C.-E., Wirtz, U., Loukianov, A.,

Rangel, P., Haberlach, G.T., Karameycheva, S.A., Tsai, J., Chiemingo, A.,

Bougl, O., Buell, C.R., Ronning, C.M., Helgeson, J., and Baker, B.

Generation of ESTs from Potato Leaves Challenged with Phytophthora

infestans, incompatible interaction (2002)

Unpublished (2002)

Contact: Robin Buell

The Institute for Genomic Research

9712 Medical Center Dr, Rockville, MD 20850, USA

Email: potato-array@tigr.org

This clone can be obtained from the University of Arizona Genomics

Institute. Orders can be made through URL:

http://genome.arizona.edu/orders/

Seq primer: T3.

Location/Qualifiers

source

1..486

/organism="Solanum tuberosum"

/mol\_type="mRNA"

/cultivar="Kennebec"

/db\_xref="taxon:4113"

/clone="BPL12K11"

/tissue\_type="leaf"

/dev\_stage="6 week old"

/lab\_host="SOLR"

/clone\_lib="P. infestans-challenged potato leaf,

incompatible reaction"

/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:

XhoI; supplier: UC Berkeley, PGEC; sequencing: the

Institute for Genomic Research. Whole plants were

challenged with 450,000 sporangia/ml P. infestans isolate

US-1 (US940501) in Biotron (Madison, Wisconsin). Leaf

tissue was collected at 1, 2, 5, 12, and 24 hours

post-challenge and frozen in liquid nitrogen immediately

upon removal. Kennebec plants showed no signs of HR.

Katanidin plants (susceptible to P. infestans US-1) were

used as controls and showed infection. NOTE: We cannot

exclude the possibility that this sequence is actually

derived from Phytophthora rather than potato."

ORIGIN

QY 3 AAGAACTTATCGAATA 18

|||||

Db 21 AAGAACTTATCGAATA 36

|||||

Query Match 76.2%; Score 16; DB 12; Length 486;

Best Local Similarity 100.0%; Pred.No. 65;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGAACTTATCGAATA 18

|||||

Db 21 AAGAACTTATCGAATA 36

|||||

Query Match 76.2%; Score 16; DB 28; Length 477;

Best Local Similarity 100.0%; Pred.No. 65;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AAGAACTTATCGAATA 19

|||||

```

ACCESSION      BE471486
VERSION        BE471486.1  GI:9561977
KEYWORDS       EST.
SOURCE         Solanum tuberosum (potato)
ORGANISM       Solanum tuberosum

REFERENCE      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS        Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                asterids; lamids; Solanales; Solanaceae; Solanum.
                1 (bases 1 to 487)
                van der Hoeven,R., Bezzerides,J., Bachem,C., Horvath,B., Visser,R.,
                Holt,I.E., Liang,F., Hansen,T.S., Utterback,T., Bowman,C.L., and
                Dean,B., Bougri,O., Buell,C.R., Ronning,C.M., Tanksley,S.D., and
                Baker,B.
                Generation of ESTs from potato swelling stolons
                Unpublished (1999)
                Contact: Robin Buell
                The Institute for Genomic Research
                9712 Medical Center Dr, Rockville, MD 20850, USA
                Email: potato-array@tigr.org
                This clone can be obtained from the University of Arizona Genomics
                Institute. Orders can be made through URL:
                http://genome.arizona.edu/orders/

FEATURES       Location/Qualifiers
                1..487
                /organism="Solanum tuberosum"
                /mol_type="mRNA"
                /cultivar="Bintje"
                /db_xref="taxon:4113"
                /clone="cST29C12"
                /tissue_type="axillary buds of stem explants, swelling
                stolons"
                /dev_stage="1 to 3 days"
                /lab_host="SOLR"
                /clone_lib="potato stolon, Cornell University"
                /note="Vector: pBlueScript SK(-); Site 1: EcoRI; Site 2:
                XhoI; RNA was supplied by Christian Bachem & Beatrix
                Horvath/Laboratory of Plant Breeding, Dept. of Plant
                Sciences, Wageningen University, The Netherlands). Total
                RNA was isolated from developing axillary buds of potato
                nodal stem cuttings cultured on medium for the
                introduction of tuber formation as described in Bachem et
                al. (Plant Journal 1996). Tissue samples were taken of
                stages corresponding to growing stolons and the early
                stages of tuber formation."

ORIGIN
Query Match      76.2%; Score 16; DB 10; Length 487;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 AAGAACTTATCGAAAT 18
        |||||
        85 AAGAACTTATCGAAAT 100

Db

RESULT 9
LOCUS    BX563981 Glossina morsitans morsitans adult infected gut Glossina
DEFINITION
BX563981
ACCESSION BX563981.1  GI:33431183
VERSION   BX563981
KEYWORDS  EST.
SOURCE    Glossina morsitans morsitans
ORGANISM  Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.
1 (bases 1 to 493)
Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune

TITLE
Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse6a02_q1c, mRNA sequence.

JOURNAL      Genome Biol. 4 (10), R63 (2003)
MEDLINE      22881942
PUBMED       14519198
COMMENT      Contact: Hall N
                Pathogen Sequencing Unit
                The Sanger Institute The Wellcome Trust Genome Campus
                Hinxton, Cambridge, CB10 1SA, UK
                Request for clones, please contact: Mike Lehane
                Prof. M.J. Lehane
                School of Biological Sciences,
                University of Wales,
                Bangor LL57 2UW
                All clones with suffix q1c are reverse primer reads starting at 5'
                end of the cDNA all plc reads are from
                the 3' end.

FEATURES       Location/Qualifiers
                1..493
                /organism="Glossina morsitans morsitans"
                /mol_type="mRNA"
                /sub_species="morsitans"
                /db_xref="taxon:37546"
                /clone="Tse6a02 q1c"
                /tissue_type="adult infected gut"
                /clone_lib="Glossina morsitans morsitans adult infected
                gut"
                /note="country: Zimbabwe; EST from adult gut infected with
                T.brucei"

ORIGIN
Query Match      76.2%; Score 16; DB 13; Length 493;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 AAGAACTTATCGAAAT 18
        |||||
        28 AAGAACTTATCGAAAT 43

Db

RESULT 10
LOCUS    BM407701 517 bp mRNA linear EST 10-MAR-2003
DEFINITION
BM407701
ACCESSION BM407701
VERSION   BM407701.1  GI:18259331
KEYWORDS  EST.
SOURCE    Solanum tuberosum (potato)
ORGANISM  Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
1 (bases 1 to 517)
van der Hoeven,R., Sun,H., Karamycheva,S.A., Tsai,J., Van Aken,S.,
Utterback,T., Chiemingo,A., Bougri,O., Buell,C.R., Ronning,C.,
Tanksley,S. and Baker,B.
Generation of ESTs from potato roots
Unpublished (2001)
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/
Seq primer: T3

FEATURES       Location/Qualifiers
                1..517
                /organism="Solanum tuberosum"
                /mol_type="mRNA"
                /cultivar="Kennebec"
                /db_xref="taxon:4113"
                /clone="cPRO32A9"

```

/tissue\_type="roots"  
/dev\_stage="in vitro grown stem cuttings"  
/lab\_host="SOLR"  
/clone\_lib="potato roots"

/note=Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; supplier: Cornell University, Tanksley lab; sequencing: The Institute for Genomic Research. Roots were isolated from in vitro grown stem cuttings on CM medium. Roots were isolated two weeks after placing the stem cuttings from in vitro grown plants on medium."

## ORIGIN

Query Match 76.2%; Score 16; DB 12; Length 517;  
Best Local Similarity 100.0%; Pred. No. 66;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGAACTTATCGAAAT 18

Db 43 AAGAACTTATCGAAAT 58

## RESULT 11

BI435938

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1. .649

/organism="Solanum tuberosum"

/mol\_type="mRNA"

/cultivar="Kennebec"

/db\_xref="taxon:4113"

/clone="cstd20L16"

/tissue\_type="dormant tuber"

/dev\_stage="one month post-harvest"

/lab\_host="SOLR"

/clone\_lib="cstd"

/note=Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; This library targets genes expressed in dormant tubers. This library was made from sections of dormant tuber, avoiding the buds and epidermis. Tubers were stored for one month post-harvest at 40C. The tuber was peeled, well away from the surface. Then it was chopped into 1-2 mm cubes and immediately frozen in liquid nitrogen. This library is noted as P4 in Tanksley lab notebooks."

Query Match 76.2%; Score 16; DB 12; Length 649;

Best Local Similarity 100.0%; Pred. No. 68;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGAACTTATCGAAAT 18

Db 43 AAGAACTTATCGAAAT 58

RESULT 13

BI435938

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1. .654

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="PI560247"

/db\_xref="taxon:39947"

/tissue\_type="coleoptile, radicle, prophyll, immature leaf"

/dev\_stage="embryo at different stages of germination and shoots of germinated seeds under chilling stress (130C/100C)"

/lab\_host="SOLR"

/clone\_lib="Rice cold stress germination cDNA library"

/note=Organ: seedlings; Vector: Lambda Uni-Zap XR excised as pBluescript; Site 1: EcoRI; Site 2: XhoI; The cDNAs were derived from reverse transcription of mRNA samples from seeds at different stages of germination and seedlings at early phase of growth under chilling stress (130C/100C). The mRNA pool was used as template for double stranded cDNA synthesis using the Stratagene Uni-Zap XR cDNA synthesis and library kit. A total of 150,000 phages were excised from the primary library as pBluescript phagemid clones. Enrichment of the primary excised library with chilling-induced transcripts was performed by hybridizing the primary excised library colony lifts with the PCR-select subtraction product, with cold germinated cDNA as tester and control temperature-germinated cDNA as driver."

Db

RESULT 12

CA998937

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1. .654

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="PI560247"

/db\_xref="taxon:39947"

/tissue\_type="coleoptile, radicle, prophyll, immature leaf"

/dev\_stage="embryo at different stages of germination and shoots of germinated seeds under chilling stress (130C/100C)"

/lab\_host="SOLR"

/clone\_lib="Rice cold stress germination cDNA library"

/note=Organ: seedlings; Vector: Lambda Uni-Zap XR excised as pBluescript; Site 1: EcoRI; Site 2: XhoI; The cDNAs were derived from reverse transcription of mRNA samples from seeds at different stages of germination and seedlings at early phase of growth under chilling stress (130C/100C). The mRNA pool was used as template for double stranded cDNA synthesis using the Stratagene Uni-Zap XR cDNA synthesis and library kit. A total of 150,000 phages were excised from the primary library as pBluescript phagemid clones. Enrichment of the primary excised library with chilling-induced transcripts was performed by hybridizing the primary excised library colony lifts with the PCR-select subtraction product, with cold germinated cDNA as tester and control temperature-germinated cDNA as driver."

Query Match 76.2%; Score 16; DB 14; Length 654;

Best Local Similarity 100.0%; Pred. No. 68;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CAAGAACTTATCGAAA 17

Db 35 CAAGAACTTATCGAAA 50

RESULT 13

BI435938

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1. .649

/organism="Solanum tuberosum"

/mol\_type="mRNA"

/cultivar="Kennebec"

/db\_xref="taxon:4113"

/clone="cstd20L16"

/tissue\_type="dormant tuber"

/dev\_stage="one month post-harvest"

/lab\_host="SOLR"

/clone\_lib="cstd"

/note=Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; This library targets genes expressed in dormant tubers. This library was made from sections of dormant tuber, avoiding the buds and epidermis. Tubers were stored for one month post-harvest at 40C. The tuber was peeled, well away from the surface. Then it was chopped into 1-2 mm cubes and immediately frozen in liquid nitrogen. This library is noted as P4 in Tanksley lab notebooks."

Query Match 76.2%; Score 16; DB 12; Length 649;

Best Local Similarity 100.0%; Pred. No. 68;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGAACTTATCGAAAT 18

Db 43 AAGAACTTATCGAAAT 58

```

B1435917      B1435917      677 bp      mRNA      linear      EST 10-MAR-2003
LOCUS      EST538678 cSTD Solanum tuberosum cDNA clone cSTD20F8 5' sequence,
DEFINITION      mRNA sequence.
ACCESSION      B1435917
VERSION      B1435917.1 GI:15260607
KEYWORDS      EST.
SOURCE      Solanum tuberosum (potato)
ORGANISM      Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE      1 (bases 1 to 677)
AUTHORS      van der Hoeven,R., Bezzerides,J., Ewing,E., Cho,J., Chiemiango,A.,
Bougr,O., Buell,C.R., Renning,C., Tanksley,S. and Baker,B.
TITLE      Generations of ESTs from dormant potato tubers
JOURNAL      Unpublished (2001)
COMMENT      Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/
Seq primer: M13F-R.
FEATURES             source
1..677
    /organism="Solanum tuberosum"
    /mol_type="mRNA"
    /cultivar="Kennebec"
    /db_xref="taxon:4113"
    /clone="cSTD20F8"
    /tissue_type="dormant tuber"
    /dev_stage="one month post-harvest"
    /lab_host="SOLR"
    /clone_lib="cSTD"
    /note="Vector: pluscript SK(-); Site_1: EcoRI; Site_2:
XhoI; This library targets genes expressed in dormant
tubers. This library was made from sections of dormant
tuber, avoiding the buds and epidermis. Tubers were stored
for one month post-harvest at 40C. The tuber was peeled,
well away from the surface. Then it was chopped into 1-2
mm cubes and immediately frozen in liquid nitrogen. This
library is noted as P4 in Tanksley lab notebooks."
ORIGIN
    Query Match      76.2%; Score 16; DB 12; Length 677;
    Best Local Similarity 100.0%; Pred. No. 69;
    Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 AAGAACTTATCGAAAT 18
      |||||
DB      90 AAGAACTTATCGAAAT 105

RESULT 14
B2387666/c
LOCUS      B2387666      685 bp      DNA      linear      GSS 30-APR-2003
DEFINITION      E1ND95TF EI_10_12_KB Entamoeba invadens genomic clone E1ND95,
genomic survey sequence.
ACCESSION      B2387666
VERSION      B2387666.1 GI:30234203
KEYWORDS      GSS
SOURCE      Entamoeba invadens
ORGANISM      Entamoeba invadens
Eukaryota; Entamoebidae; Entamoeba.
REFERENCE      1 (bases 1 to 685)
AUTHORS      Wang,Z., Samuelson,J., Clark,C.G., Eichinger,D., Paul,J., van
Dellen,K., Hall,N., Anderson,I. and Loftus,B.
TITLE      Gene discovery in the Entamoeba invadens genome
JOURNAL      Mol. Biochem. Parasitol. 129 (1), 23-31 (2003)
MEDLINE      22684048
PUBMED      12798503

```

```

Other GSSs: E1ND95STR
Contact: Brendan Loftus
Department of Eukaryotic Genomics
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: enta@tigr.org
DNA was provided by Daniel Eichinger
Seq primer: TF
Class: Sheared ends.
Location/Qualifiers
1..685
    /organism="Entamoeba invadens"
    /mol_type="genomic DNA"
    /strain="IP-1"
    /db_xref="taxon:33085"
    /clone="E1ND95"
    /note="Vector: PHOS2; Site_1: BstXI; Total genomic DNA was
isolated from early log phase trophozoites of E. invadens
IP-1 using a Qiagen plant DNA extraction kit. A shotgun
medium-size plasmid library (average insert size of 10 -
12 kb) was generated by random mechanical shearing of E.
invadens genomic DNA, repairing the ends of DNA fragments
with T4 Polymerase, adding BstXI adaptors and ligating
into the BstXI site of a pUC-derived vector PHOS2."
ORIGIN
    Query Match      76.2%; Score 16; DB 28; Length 685;
    Best Local Similarity 100.0%; Pred. No. 69;
    Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 AAGAACTTATCGAAAT 18
      |||||
DB      22 AAGAACTTATCGAAAT 7

RESULT 15
BG031536
LOCUS      BG031536      694 bp      mRNA      linear      EST 24-JAN-2001
DEFINITION      602299367F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:4393720 5',
mRNA sequence.
ACCESSION      BG031536
VERSION      BG031536.1 GI:12421916
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 694)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10088 row: e column: 17
High quality sequence stop: 612.
Location/Qualifiers
1..694
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="IMAGE:4393720"
    /tissue_type="mammary adenocarcinoma, cell line"
    /lab_host="DH10B (phage-resistant)"
FEATURES             source
1..694
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="IMAGE:4393720"
    /tissue_type="mammary adenocarcinoma, cell line"
    /lab_host="DH10B (phage-resistant)"

```

```
/clone_lib="NIH_MGC_87"  
/note="Organ: breast; Vector: pCMV-SPORT6; Site 1: NotI;  
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.  
Average insert size 1.383 kb. Library enriched for  
full-length clones and constructed by Life Technologies.  
Note: this is a NIH_MGC Library."
```

## ORIGIN

```
Query Match      76.2%; Score 16; DB 10; Length 694;  
Best Local Similarity 100.0%; Pred. No. 69;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      3  AGAAGCTTATCGAAT 18  
         |||||  
Db      469 AGAAGCTTATCGAAT 484
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Search completed: August 2, 2004, 20:28:09  
Job time : 871.879 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 2, 2004, 19:08:00 ; Search time 106.267 Seconds  
(without alignments)  
968.934 Million cell updates/sec

Title: US-10-068-067-19

Perfect score: 21  
Sequence: 1 gcaagaacttcgaaataca 21

Scoring table: OIRGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 3222919 seqs, 2451570024 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6445838

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA:  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:  
9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:  
10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:  
11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:  
12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:  
13: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq2:  
14: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:  
15: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:  
16: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:  
17: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:  
18: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:  
19: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	21	14	US-10-068-067-19
2	21	100.0	21	14	Sequence 19, Appl
3	21	100.0	51	14	Sequence 24, Appl
4	21	100.0	51	14	Sequence 16, Appl
5	21	100.0	1193	15	Sequence 21, Appl
6	21	100.0	2895	14	US-10-068-067-21
7	17	81.0	11124	14	Sequence 3, Appl
8	17	81.0	11184	14	Sequence 11, Appl
9	16	76.2	465	17	Sequence 286, Appl
10	16	76.2	1761	17	Sequence 284, Appl
11	15	71.4	537	10	Sequence 67946, A
12	15	71.4	1500	16	Sequence 67947, A
13	15	71.4	1556	17	Sequence 1052, A
14	15	71.4	1674	9	Sequence 46193, A
					Sequence 52116, A
					Sequence 665, Appl

c	15	71.4	1674	11	US-09-938-842A-665	Sequence 665, App
	16	66.7	158	13	US-10-424-599-86155	Sequence 86155, A
c	17	66.7	247	17	US-10-437-963-30059	Sequence 30059, A
	18	66.7	479	13	US-10-240-425-1360	Sequence 1360, Ap
	19	66.7	495	13	US-10-027-632-94597	Sequence 94597, A
	20	66.7	495	13	US-10-027-632-305493	Sequence 305493, A
	21	66.7	495	16	US-10-027-632-94597	Sequence 94597, A
	22	66.7	495	16	US-10-027-632-305493	Sequence 305493, A
c	23	66.7	564	13	US-10-282-122A-17492	Sequence 17492, A
c	24	66.7	575	13	US-10-424-599-76184	Sequence 76184, A
	25	66.7	672	9	US-09-770-149-565	Sequence 565, App
	26	66.7	714	13	US-10-282-122A-38551	Sequence 38551, A
c	27	66.7	714	13	US-10-424-599-107802	Sequence 107802, A
	28	66.7	898	10	US-09-841-260-138	Sequence 138, App
	29	66.7	898	14	US-10-007-693-138	Sequence 138, App
	30	66.7	898	17	US-10-762-058-138	Sequence 138, App
	31	66.7	1023	16	US-10-369-493-44068	Sequence 44068, A
	32	66.7	1026	16	US-10-369-493-30362	Sequence 25003, A
	33	66.7	1079	16	US-10-369-493-30362	Sequence 30362, A
	34	66.7	1338	13	US-10-282-122A-12435	Sequence 12435, A
	35	66.7	1366	13	US-10-282-122A-37797	Sequence 37797, A
c	36	66.7	1848	17	US-10-437-963-102418	Sequence 102418, A
c	37	66.7	2177	16	US-10-447-515-3	Sequence 3, Appli
	38	66.7	2238	13	US-10-424-599-2236	Sequence 2236, Ap
c	39	66.7	2354	10	US-09-841-260-137	Sequence 137, App
c	40	66.7	2354	14	US-10-007-693-137	Sequence 137, App
c	41	66.7	2354	17	US-10-762-058-137	Sequence 137, App
	42	66.7	2424	16	US-10-369-493-45830	Sequence 45830, A
	43	66.7	3674	17	US-10-437-963-83590	Sequence 83590, A
c	44	66.7	3900	17	US-10-437-963-88074	Sequence 88074, A
	45	66.7	4820	13	US-10-158-844-19	Sequence 19, Appl

#### ALIGNMENTS

RESULT 1  
US-10-068-067-19  
; Sequence 19, Application US/10068067  
; Publication No. US20020151064A1  
; GENERAL INFORMATION:  
; APPLICANT: Rothenberg, Marc E.  
; APPLICANT: Zimmermann, Nives  
; APPLICANT: Children's Hospital Medical Center  
; TITLE OF INVENTION: REGULATION OF CCR3 EXPRESSION  
; FILE REFERENCE: CMC-153  
; CURRENT APPLICATION NUMBER: US/10/068, 067  
; CURRENT FILING DATE: 2002-02-05  
; PRIOR APPLICATION NUMBER: 60/267,073  
; PRIOR FILING DATE: 2001-02-07  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 19  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-068-067-19

Query Match 100.0%; Score 21; DB 14; Length 21;  
Best Local Similarity 100.0%; Pred. No. 0.0077;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGAAGCTTATCGAAATACA 21  
Db 1 GCAAGAAGCTTATCGAAATACA 21

RESULT 2  
US-10-068-067-24  
; Sequence 24, Application US/10068067  
; Publication No. US20020151064A1  
; GENERAL INFORMATION:  
; APPLICANT: Rothenberg, Marc E.





Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGAACTTATCGAATAACA 21  
Db 15 GCAAGAACTTATCGAATAACA 35

## RESULT 6

US-10-068-067-11  
; Sequence 11, Application US/10068067  
; Publication No. US20020151064A1  
; GENERAL INFORMATION:  
; APPLICANT: Rothenberg, Marc E.  
; APPLICANT: Zimmermann, Nives  
; APPLICANT: Children's Hospital Medical Center  
; TITLE OF INVENTION: REGULATION OF CCR3 EXPRESSION  
; FILE REFERENCE: CMC-153  
; CURRENT APPLICATION NUMBER: US/10/068,067  
; CURRENT FILING DATE: 2002-03-27  
; PRIOR APPLICATION NUMBER: 60/267,073  
; PRIOR FILING DATE: 2001-02-07  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 11  
; LENGTH: 2895  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-068-067-11

Query Match 100.0%; Score 21; DB 14; Length 2895;

Best Local Similarity 100.0%; Pred. No. 0.0098; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGAACTTATCGAATAACA 21  
Db 1591 GCAAGAACTTATCGAATAACA 1611

## RESULT 7

US-10-108-605-286/c  
; Sequence 286, Application US/10108605  
; Publication No. US20020160934A1  
; GENERAL INFORMATION:  
; APPLICANT: Broadus, Julie  
; APPLICANT: Stam, Lynn  
; APPLICANT: Bachmann, Jane  
; APPLICANT: Kamdar, Kim  
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE  
; FILE REFERENCE: 31133B  
; CURRENT APPLICATION NUMBER: US/10/108,605  
; CURRENT FILING DATE: 2002-03-27  
; PRIOR APPLICATION NUMBER: US 09/761,142  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/176,418  
; PRIOR FILING DATE: 2000-01-14  
; NUMBER OF SEQ ID NOS: 361  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 286  
; LENGTH: 11124  
; TYPE: DNA  
; ORGANISM: Drosophila melanogaster  
US-10-108-605-286

Query Match 81.0%; Score 17; DB 14; Length 11124;

Best Local Similarity 100.0%; Pred. No. 2.5; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGAACTTATCGAATAACA 19  
Db 3529 AAGAACTTATCGAATAACA 3513

## RESULT 8

US-10-108-605-284/c  
; Sequence 284, Application US/10108605  
; Publication No. US20020160934A1  
; GENERAL INFORMATION:  
; APPLICANT: Broadus, Julie  
; APPLICANT: Stam, Lynn  
; APPLICANT: Bachmann, Jane  
; APPLICANT: Kamdar, Kim  
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE  
; FILE REFERENCE: 31133B  
; CURRENT APPLICATION NUMBER: US/10/108,605  
; CURRENT FILING DATE: 2002-03-27  
; PRIOR APPLICATION NUMBER: US 09/761,142  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/176,418  
; PRIOR FILING DATE: 2000-01-14  
; NUMBER OF SEQ ID NOS: 361  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 284  
; LENGTH: 11184  
; TYPE: DNA  
; ORGANISM: Drosophila melanogaster  
US-10-108-605-284

Query Match 81.0%; Score 17; DB 14; Length 11184;

Best Local Similarity 100.0%; Pred. No. 2.5; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAGAACTTATCGAATAACA 19  
Db 3589 AAGAACTTATCGAATAACA 3573

## RESULT 9

US-10-437-963-67946  
; Sequence 67946, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 67946  
; LENGTH: 465  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_68757C.1  
US-10-437-963-67946

Query Match 76.2%; Score 16; DB 17; Length 465;

Best Local Similarity 100.0%; Pred. No. 8.5; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CAAGAACTTATCGAAA 17  
Db 120 CAAGAACTTATCGAAA 135

## RESULT 10

US-10-437-963-67947/c

```
; Sequence 67947, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 46193
; LENGTH: 1500
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-46193

Query Match 71.4%; Score 15; DB 16; Length 1500;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGAACTTATCGA 15
DB 237 GCAGAACTTATCGA 251

RESULT 13
US-10-437-963-52116
; Sequence 52116, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 52116
; LENGTH: 1556
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_54443C.1
US-10-437-963-52116

Query Match 71.4%; Score 15; DB 17; Length 1556;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CAAGAACTTATCGAA 16
DB 777 CAAGAACTTATCGAA 791

RESULT 14
US-09-938-842A-665/c
; Sequence 665, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun

; Sequence 67947, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 67947
; LENGTH: 1761
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_68758C.1
US-10-437-963-67947

Query Match 76.2%; Score 16; DB 17; Length 1761;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CAAGAACTTATCGAAA 17
DB 1265 CAAGAACTTATCGAAA 1250

RESULT 11
US-09-991-936-1052
; Sequence 1052, Application US/09991936
; Publication No. US20030073827A1
; GENERAL INFORMATION:
; APPLICANT: Brandt, Kevin S.
; APPLICANT: Gaines, Patrick J.
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: FLEA HEAD, NERVE CORD, HINDGUT AND MALPIGHIAN TUBULE
; FILE REFERENCE: PC-6-C1
; CURRENT APPLICATION NUMBER: US/09/991,936
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US/09/543,668
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/128,704
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1959
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1052
; LENGTH: 537
; TYPE: DNA
; ORGANISM: Ctenocephalides felis
US-09-991-936-1052

Query Match 71.4%; Score 15; DB 10; Length 537;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AACTTATCGAATAC 20
DB 144 AACTTATCGAATAC 158

RESULT 12
US-10-369-493-46193
; Sequence 46193, Application US/10369493
; Publication No. US20030233675A1
```

; APPLICANT: Zhu, Tong  
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
; TITLE OF INVENTION: SAME, AND METHODS OF USE  
; FILE REFERENCE: SRIPI300-3  
; CURRENT APPLICATION NUMBER: US/09/938,842A  
; CURRENT FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: US 60/227,866  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US 60/264,647  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/300,111  
; PRIOR FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 5379  
; SEQ ID NO 665  
; LENGTH: 1674  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-938-842A-665

Query Match 71.4%; Score 15; DB 9; Length 1674;  
Best Local Similarity 100.0%; Pred.No.35;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AACTTATCGAAATAC 20  
|||  
DB 563 AACTTATCGAAATAC 549

RESULT 15  
US-09-938-842A-665/c  
; Sequence 665, Application US/09938842A  
; Publication No. US20040009476A9  
; GENERAL INFORMATION:  
; APPLICANT: Harper, Jeff  
; APPLICANT: Kreps, Joel  
; APPLICANT: Wang, Xun  
; APPLICANT: Zhu, Tong  
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
; TITLE OF INVENTION: SAME, AND METHODS OF USE  
; FILE REFERENCE: SRIPI300-3  
; CURRENT APPLICATION NUMBER: US/09/938,842A  
; CURRENT FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: US 60/227,866  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US 60/264,647  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/300,111  
; PRIOR FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 5379  
; SEQ ID NO 665  
; LENGTH: 1674  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-938-842A-665

Query Match 71.4%; Score 15; DB 11; Length 1674;  
Best Local Similarity 100.0%; Pred.No.35;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AACTTATCGAAATAC 20  
|||  
DB 563 AACTTATCGAAATAC 549

Search completed: August 2, 2004, 22:36:37  
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